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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 15:47:39 ; Search time 313.62 Seconds
(without alignments)
7887.743 Million cell updates/sec

Title: US-09-292-411a-1
Perfect score: 771
Sequence: 1 atgttaaatcttgaaacaa.....gattccacgcaataataaa 771

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2138461 seqs, 1604250230 residues

Total number of hits satisfying chosen parameters: 4276922

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA_New.*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	767.6	99.6	774	7 US-10-089-019-11	Sequence 11, Appl
2	761	98.7	916	7 US-10-138-701-5	Sequence 5, Appl
3	325.6	42.2	777	8 US-60-360-039-40175	Sequence 40175, A
4	286.8	37.2	783	8 US-60-360-039-41051	Sequence 41051, A
5	247.8	32.1	810	8 US-60-360-039-41383	Sequence 41383, A
6	224.6	29.1	792	8 US-60-360-039-42526	Sequence 42526, A
7	222.2	28.8	780	8 US-60-360-039-43741	Sequence 43741, A
8	191.6	24.9	753	8 US-60-360-039-42031	Sequence 42031, A
9	182.2	23.6	837	8 US-60-360-039-26327	Sequence 26327, A
10	150.6	19.5	786	8 US-60-360-039-24075	Sequence 24075, A
11	140	18.2	889	5 US-09-882-227-493	Sequence 493, App
12	137.8	17.9	786	8 US-60-360-039-44878	Sequence 44878, A
13	133	17.3	768	8 US-60-360-039-43253	Sequence 43253, A
14	129.2	16.8	783	8 US-60-360-039-35437	Sequence 35437, A
15	129.2	16.8	783	8 US-60-360-039-37978	Sequence 37978, A
16	129.2	16.8	783	8 US-60-360-039-38173	Sequence 38173, A
17	129.2	16.8	783	8 US-60-360-039-38557	Sequence 38557, A
18	127	16.5	780	8 US-60-360-039-33737	Sequence 33737, A
19	122.6	15.9	819	8 US-60-360-039-35974	Sequence 35974, A
20	121.8	15.8	789	7 US-10-089-019-23	Sequence 23, Appl
21	121.8	15.8	789	8 US-60-360-039-24499	Sequence 24499, A
22	119.8	15.5	792	8 US-60-360-039-37477	Sequence 37477, A
23	119.2	15.4	762	8 US-60-360-039-44299	Sequence 44299, A
24	118.4	15.4	762	8 US-60-360-039-41596	Sequence 41596, A
25	112.6	14.6	858	8 US-60-360-039-23801	Sequence 23801, A

ALIGNMENTS

RESULT 1

US-10-089-019-11
; Sequence 11, Application US/10089019
; GENERAL INFORMATION:
; APPLICANT: DEMOLF, WALTER E. JR
; APPLICANT: KALLENDER, HOWARD
; APPLICANT: LONSDALE, JOHN T.
; TITLE OF INVENTION: METHODS FOR MAKING AND USING FATTY ACID
; TITLE OF INVENTION: SYNTHESIS PATHWAY REAGENTS
; FILE REFERENCE: GM50068
; CURRENT APPLICATION NUMBER: US/10/089,019
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/US00/29451
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/161,775
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-089-019-11

Query Match 99.6%; Score 767.6; DB 7; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.1e-179;
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	ttaaatcttgaaacaaacataatgtcatcgtaataagcgtagtattgct 63
Db	7	ttaaatcttgaaacaaacataatgtcatcgtaataagcgtagtattgct 66
QY	64	tttggtcgctaaagtcttagatcaattagtgctaaatagttactaccgtaaa 123
Db	67	tttggtcgctaaagtcttagatcaattagtgctaaatagttactaccgtaaa 126
QY	124	gaacgtagcgttaaagagcttgaaaaattattagaacaattaaatcaacagagcgac 183
Db	127	gaacgtagcgttaaagagcttgaaaaattattagaacaattaaatcaacagagcgac 186
QY	184	ttatataaattgattgttcaaacgcatgaagaggttatttaattgttttgagcaaatggt 243
Db	187	ttatataaattgattgttcaaacgcatgaagaggttatttaattgttttgagcaaatggt 246
QY	244	aaagatgttgcccaattgattgtgtatcatcattgcatttgcataatggaagac 303
Db	247	aaagatgttgcccaattgattgtgtatcatcattgcatttgcataatggaagac 306

Qy	304	ttacgcgacgctttcttctgaaacttcaacgtaagggtctcttgtagctcaagacattagt	363
Db	307	ttacgcgacgctttcttctgaaacttcaacgtaagggtctcttgtagctcaagacattagt	366
Qy	364	tcttactcattacaatttggtctcatgaagctcaaaaaataatgccaagaagtggtgac	423
Db	367	tcttactcattacaatttggtctcatgaagctcaaaaaataatgccaagaagtggtgac	426
Qy	424	attgtgtcaacaacatatattaggtggtcgaaattcgcaggttcaaaattataatgtgatgggt	483
Db	427	attgtgtcaacaacatatattaggtggtcgaaattcgcaggttcaaaattataatgtgatgggt	486
Qy	484	gttgttaaacgagcttagaagcaaatgtttaaatatttagcattagacttagtctctgat	543
Db	487	gttgttaaacgagcttagaagcaaatgtttaaatatttagcattagacttagtctctgat	546
Qy	544	aattatcgcgttaatgcaattcagctggttccaaatcgttacattaaagtgcataaagggtgtg	603
Db	547	aattatcgcgttaatgcaattcagctggttccaaatcgttacattaaagtgcataaagggtgtg	606
Qy	604	ggtggtttcaatacaattcttaagaataatcgaaagcgtgtgcaccttataaaacgttaacgtt	663
Db	607	ggtggtttcaatacaattcttaagaataatcgaaagcgtgtgcaccttataaaacgttaacgtt	666
Qy	664	gatcaagtacgaagttagtataaacacgagcgttactttrttaagtgactttacaagtggcggt	723
Db	667	gatcaagtacgaagttagtataaacacgagcgttactttrttaagtgactttacaagtggcggt	726
Qy	724	acagggtgaaaattattcatgtagatagcggattccacgcaattataataa	771
Db	727	acagggtgaaaattattcatgtagatagcggattccacgcaattataataa	774

RESULT 2

US-10-138-701-5

; Sequence 5, Application US/10138701

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides

; FILE REFERENCE: PR404

; CURRENT APPLICATION NUMBER: US/10/138,701

; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: US/09/512,255A

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/098,964

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: US 60/009,861

; PRIOR FILING DATE: 1996-01-05

; PRIOR APPLICATION NUMBER: PCT/ US99/19726

; PRIOR FILING DATE: 1999-08-31

; PRIOR APPLICATION NUMBER: US 08/956,171

; PRIOR FILING DATE: 1997-10-20

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 916

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-138-701-5

Qy	121	aaagaacgtgacgcgttaaaagagcttgaaaaattattagaaacaattaaatacaaccagaagcg	180
Db	216	aaagaacgtgacgcgttaaaagagcttgaaaaattattagaaacaattaaatacaaccagaagcg	275
Qy	181	cacttatatacaaatgtatgttccaaagcgatgaagagaggtattaatggtttttgagcaaat	240
Db	276	cacttatatacaaatgtatgttccaaagcgatgaagagaggtattaatggtttttgagcaaat	335
Qy	241	ggtaaagatgttgccaataattgatgggtgtatatacattcaatcgacttctgctaatacggaa	300
Db	336	ggtaaagatgttgccaataattgatgggtgtatatacattcaatcgacttctgctaatacggaa	395
Qy	301	gacttacgcggacgctttctgaaacttcacgtgaaggcttctgttagctcaagacatt	360
Db	396	gacttacgcggacgctttctgaaacttcacgtgaaggcttctgttagctcaagacatt	455
Qy	361	agttcttactcattaaacaattgtggtcattgaagcttaaaaaataatgccagaagtggt	420
Db	456	agttcttactcattaaacaattgtggtcattgaagcttaaaaaataatgccagaagtggt	515
Qy	421	agcaattgttcaacaacacatatttagtggcggaatttcgcagttccaaaattataatgtgatg	480
Db	516	agcaattgttcaacaacacatatttagtggcggaatttcgcagttccaaaattataatgtgatg	575
Qy	481	gggtgtgtctaaagcgagcttagaagcaaatgtttaaattatttagcatttagacttagtgctt	540
Db	576	gggtgtgtctaaagcgagcttagaagcaaatgtttaaattatttagcatttagacttagtgctt	635
Qy	541	gataatattcggttaattgcaatttcagctggttccaatccgtacattaaagtgcataaaggt	600
Db	636	gataatattcggttaattgcaatttcagctggttccaatccgtacattaaagtgcataaaggt	695
Qy	601	gtgggtgtgttccaatacaattcttaagaagaatcgaaagcggtgcaccttataaacgtaac	660
Db	696	gtgggtgtgttccaatacaattcttaagaagaatcgaaagcggtgcaccttataaacgtaac	755
Qy	661	gttgatcaagtagaagtagtgtaaaacagcggtctacttrttaagtgaactatacaagtggc	720
Db	756	gttgatcaagtagaagtagtgtaaaacgctggcgttacttataagtgattatacaagtggc	815
Qy	721	gttacaggtgaaaatactcatgtagatagcgattccacgcaattataaa	771
Db	816	gttacaggtgaaaatactcatgtagatagcgattccacgcaattataaa	866
RESULT 3			
US-60-360-039-40175			
; Sequence 40175, Application US/60360039			
; GENERAL INFORMATION:			
; APPLICANT: Cao, Yongwei			
; APPLICANT: Chen, Xianfeng			
; APPLICANT: Goldman, Barry S.			
; APPLICANT: Hinkle, Gregory J.			
; APPLICANT: Slater, Steven C.			
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODU			
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES			
; FILE REFERENCE: 38-10(52052)A			
; CURRENT APPLICATION NUMBER: US/60/360,039			
; CURRENT FILING DATE: 2002-02-21			
; NUMBER OF SEQ ID NOS: 47374			
; SEQ ID NO 40175			
; LENGTH: 777			
; TYPE: DNA			
; ORGANISM: Bacillus thuringiensis			
US-60-360-039-40175			

Query Match 98.7%; Score 761; DB 7; Length 916;
Best Local Similarity 99.1%; Pred. No. 4.8e-178;
Matches 764; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 16 atggaactattacaagggaaaacatttgggtatggcggtgcgaacaaaagatt 75
QY 61 gctttgtgtgctaaagtatttagatcaattagggtgctaaatttagtatttaccgt 120
Db 76 gcatgggaatagctcgtcttgcataatgcaggtgcaaaatttaattcatatgca 135
QY 121 aaagaacgtagcgcgttaaagagcttgaataattattagaacaattaaatcaacagaagcg 180
Db 136 ggagaacgtttgaagaacgttcgtgaattagcgcacatttagaaggacaagaatca 195
QY 181 cacttatatacaattgatgttcaagcgaatgaagaggttatttaagtgttttagcaaaatt 240
Db 196 cctgtattacccttgatgttaacgaatgatgggaacttacagcttgccttgaacaatt 255
QY 241 ggttaagaatgttggcaaatatgatgtgtatcatcattcattcgtcatttgcataatggaa 300
Db 256 aaacaagaatgtagtactattcacggttagcacattgtattgtctttgcaaatgcgat 315
QY 301 gacttacgagcgtctttctgaacacttcacgtgaagcgttcttctgttagctcaagaacatt 360
Db 316 gacttaaaaggtgaatttagatactctcgcgattggtatttttacttgcacaaaatt 375
QY 361 agtttactacttaacaatttgctcatgaagctaaataaataatgaagcagaagtggt 420
Db 376 agcgcattctcttaacagcttagcaagaagcgaaggaagatgacagaagcgga 435
QY 421 agcattgttgcacaacatatattaggtggtgaattcgcagttcacaataattatattgtgatg 480
Db 436 aatatttaacataacataccttggcgcgagcgttggtaaaattataacgttatg 495
QY 481 ggtgtgtcaagcagcgttagaagcaaatgttaaatatttagcatttagcttagtct 540
Db 496 ggtgtgtcgaagcgttcatttagaagcagcgtgaatatttagcgaacgatttagtcaa 555
QY 541 gataatattcgtgttaattcaattcagctgttccaaatcgttacatttaagtcgaaggt 600
Db 556 cagcgtattcgtgttaacgctattctgcaggaccaattcgtacgttattcgtcaaaaggt 615
QY 601 gttgggtgttcaatacacaattcttaagaatacgaagcgtgacgtttaaacaagtaac 660
Db 616 gtaggcgattcaactcaacttaagagaattgagagcgcgaccacttgcgtaca 675
QY 661 gttgatcaagtagaagtagttaaagcagcgttactttrtaagtgaacttatcaagtgc 720
Db 676 acaacgcaagaaggttgcgatacagcagtagtattcttacttactttagcagcgtg 735
QY 721 gttacaggtgaataattcatagatagcgaattcca 758
Db 736 gtaacagggaagaacattcatgtgattcagggatca 773

RESULT 4

US-60-360-039-41051
; Sequence 41051, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 41051

; LENGTH: 783

; TYPE: DNA

; ORGANISM: Bacillus halodurans

US-60-360-039-41051

Query Match 37.2%; Score 286.8; DB 8; Length 783;
Best Local Similarity 61.8%; Pred. No. 4e-61;
Matches 456; Conservative 0; Mismatches 282; Indels 0; Gaps 0;

QY 22 acatatgtcatcatcgaatcgctaaataagcgtagtagtctgttcttgggtcgtcaaatgtt 81
Db 28 acatatgtgtcatggcgctgcacaataagcgtagcattgcttggggaattgctcagtc 87
QY 82 ttatgacaattaggtgctaaattagtagtatttacttaccgttaaagaacgttagccgaagag 141
Db 88 ctagccaattgcagggaacaggcgtgatttttacgtatgcggggaagcgttagtgagaaaat 147
QY 142 ctgaaaaattattagaacaattaaatcaaccagaagcgcacttatatacaaaattgtgtt 201
Db 148 gttagaggatttagtgaaacgcttagacggtgtagtcacacctcgtatttagagtgatgtg 207
QY 202 caaagcgtgaagaggttatttaattggttttgagcaaaattggttaaaagatgttgcaaatatt 261
Db 208 acaagtgtatgaagccgttgaagcaacatttgcgagcatcaagaggaagcgaattggcaaat 267
QY 262 gatgtgttatcatcaatcgcatttgcataatggaagcacttagcgcgacgtctttct 321
Db 268 catggattggtcactgcgtcgttttgcataaagagaggttagaaggggagtattta 327
QY 322 gaaacttcagtgaaaggcttctttagctcaagacattagttcttacttactcatacaaat 381
Db 328 aatacgcactgcgtggtcttttatttagctcacaatatatttagtcatactctttgacggt 387
QY 382 gtagctcatgaagcgtcaaaaatttaagcagaaggtggttagcatttggcaacaacatat 441
Db 388 gtggcgaagcggcccgctcgcctcatgaacgaaggaaggaacgctaaacactactat 447
QY 442 ttagggtggcgaattcgcagttcacaattataatgtaggtgtgtgttcttaaagcgactta 501
Db 448 ttaggcgggtgaaaaattgtccgttaataatcattgtttatggcgcagcgaaggcgtctct 507
QY 502 gaagcaaatgttaattatttagcatttagccttaggttctgataataattcgcgttaattgca 561
Db 508 gacgcaagcgtaaagtatttagcaacgactcttgcaaggaacacattcgcgttaaacgct 567
QY 562 atttcagcgtggtccatccgtacattaaagtgcgaaggtggtgggtgttttcaatacaatt 621
Db 568 atttcgcgtggaacgtacccgaccccttgcgcgaaggaatcgcggttcaatgacgtc 627
QY 622 cttaagaataatcgaagcgtgcacctttaaacaacgttagcattcaagttagagtaggt 681
Db 628 ttaaggaataatcgaagagcgtgcaccactccgcgaacacactacgaagaagtaggg 687
QY 682 aaaaacgcggttacttrttaagtgaacttatcaagtggcgttacaggtgaaaaattcat 741
Db 688 gatactgcattgttctcgtagtgacctttcaagaggaatcacaaggggaattttacac 747
QY 742 gtatagagcggattccac 759
Db 748 gtatagcgcgataaac 765

RESULT 5

US-60-360-039-41383

; Sequence 41383, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

QY 669 agtagaagtaggtataaagcggcgttactttrttaagtgaactatacaagtggcggttacagg 728
Db 654 tdatgatgtgggtcaactgcgccttctctgttagcccaactgctcaggtgtcatagg 713
QY 729 tgaataatcatgtagatagcggattccacgcaataaa 768
Db 714 tgatatcgtttatgtgtataaagggttccatttaacataa 753

RESULT 9
US-60-360-039-26327
; Sequence 26327, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 26327
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Synechocystis sp.
US-60-360-039-26327

Query Match 23.6%; Score 182.2; DB 8; Length 837;
Best Local Similarity 53.4%; Pred. No. 2.5e-35;
Matches 404; Conservative 1; Mismatches 349; Indels 3; Gaps 1;

QY 1 atgttaaatcttgaaacaaacatatgtcatcattggaatcggttaataaagcgtagtatt 60
Db 61 atgttagatctcagcggcaagcaagccttgttaccggcatcgccaataatcgctccatt 120
QY 61 gcttttggtgcgttaagatttttagatcaattagtgctgtataattagttacttaccgt 120
Db 121 gcctgggcatggcccaacactacacagccggggctgaaatggcggttagttattt 180
QY 121 aaagacatagcgttaagagcttgaaataattattagacaataaa---tcaacagaa 177
Db 181 ccagatgagaaggcagatttgaaagaaagtgcgggagtgaccagacgttgcacct 240
QY 178 gcgcacttatcaaatgatgttcaaaagcagatgaagaggttattaaatggtttgagcaa 237
Db 241 accctcgtctgcgggggacgtacagacgatgccagggtggatgccctgttccatagc 300
QY 238 atggtaaaagatttggcaaatatgatgggtgtatatacttaactcgaatttgctaattg 297
Db 301 gtaaggaaaaatgggcaaaactcgatatttgcacattccttagccttgcgcgacaag 360
QY 298 gaagacttaacgcgacgctttcttgaaacttcaagtgaggctcttctgttagctcaagac 357
Db 361 tccggtttgacgggaattataccgatattcccaaggagccttttagtcaagcaatggaa 420
QY 358 attagttctactcattaaacattgtggtcattgaagctaaataaattaatgccagaaggt 417
Db 421 attagcactattccctggcggttggctcgggggcaaaccccttgatgaccaatggc 480
QY 418 ggtagcattgttgcaacacatatatttagtggcgaaattcgcagttcgaataataatgtg 477
Db 481 ggtagcattacacctgaacttacttttggcgcggtgaaggttattcccaactacaacctg 540
QY 478 atgggtgtgtcaagcagctttagaagcaaaatgttaaatattbagcattagattaggt 537
Db 541 atgggggtggcgaaggccggtctggaaatgactgtgcgttatctggcgcgagaattgggg 600
QY 538 cctgataatctgcgttaattgcaatttcagctgttccaatccgtacattaaatgagcaaaa 597

Db 601 ccccaaatattcgtgttaatttccgtgttccgtggcccatccgcgacccctgcttctcg 660
QY 598 ggtgtgggtgttcaatacaattcttaagaaatcgaagacgctgcacctttaaact 657
Db 661 gcgggtgggggcatattttggatattccaccatgtggaagaggtggcaccactaaagct 720
QY 658 aacgtttgatcagtagaagtagtaaaacagcggttactttrttaagtgaacttataagt 717
Db 721 accgtcacccaaacggaagtgggaatacacagcggttctctggccagtgacctttccagt 780
QY 718 ggcgttacaggtgaaataattcatatagatagcggat 754
Db 781 ggcattaccggacaattatctacgtcgtcttctggct 817

RESULT 10
US-60-360-039-24075
; Sequence 24075, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 24075
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Xenorhabdus nematophilus
US-60-360-039-24075

Query Match 19.5%; Score 150.6; DB 8; Length 786;
Best Local Similarity 52.3%; Pred. No. 1.5e-27;
Matches 383; Conservative 1; Mismatches 340; Indels 9; Gaps 2;

QY 27 tgtcatcattgggaatcgcttaataagcgttagtattgttcttgggtcgctaaagtatttaga 86
Db 27 tctaatcctggcgtgccagcaaaactgtctattgtctatggaattggcgaagcaatgca 86
QY 87 tcaattagtgctaaattagttacttaccgttaaaagacgtagccgtaaagagcttga 146
Db 87 cgacaagggtgcagaactggcttttaccctaccagaatgacaaaattgaaacctcgtgtga 146
QY 147 aaattattagaacaaattaaatcaaccagagcgacttatcaataatgattgttcaaaag 206
Db 147 agaattcgacatctctgaattcacaacatcgttctgcacgtcgacgtggctc-----a 200
QY 207 cgatgaagaggttattaatgttttgagcaaaattgggtaaagatgttggcaatattgctgg 266
Db 201 agatgaagatcgcacacattgttctgtgaactgggttaaagtatggcgaataatgctgg 260
QY 267 tgtatcatcaatcgcatttgcataatggaagacttac---gcggacacttttttga 323
Db 261 tttgttcactctatcgtgttatgccccgcgaaacacttgcattggtgcgttcaatgctg 320
QY 324 aacttcactgaaaggcttctgttagctcaagacattagttcttactcatcaacaaatgt 383
Db 321 cgtcagcgtgaaaggtttcaaaatagcacatgatcatcagcgacatacagcttgcgcatt 380
QY 384 ggcctgaagactaaaaaattaaatgcaagaggtgtgtagcattgttggcaacaaacatttt 443
Db 381 ggcaaaagcattgctgtagtattgtaacctgactcagcgtcgtctaaactttaaactttt 440
QY 444 aggtggcgaaattcgcagttcaaaattataatgtgatgggtgttgcataaagcgagcttaga 503
Db 441 aggtgcgagagcgtgcaatccctaaactacacgtgtatgggattagcaaaagcttctctgga 500

[illegible]

```

RESULT 11
US-09-882-227-493
: Sequence 493, Application US/09882227
: GENERAL INFORMATION:
: APPLICANT: Kleanthous, Harold
: APPLICANT: Al-Garawi, Amal
: APPLICANT: Miller, Charles
: APPLICANT: Tomb, Jean-Francois
: APPLICANT: Ooomen, Raymond P.
: TITLE OF INVENTION: Identification of polynucleotides
: TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides in the Helicobacter
: TITLE OF INVENTION: Genome
: FILE REFERENCE: 06132/047002
: CURRENT APPLICATION NUMBER: US/09/882.227
: CURRENT FILING DATE: 2001-06-15
: PRIOR APPLICATION NUMBER: US 08/902,615
: PRIOR FILING DATE: 1997-07-29
: NUMBER OF SEQ ID NOS: 638
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 493
: LENGTH: 889
: TYPE: DNA
: ORGANISM: Helicobacter pylori
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (16)...(840)
US-09-882-227-493

```

Query Match	18.2%;	Score 140;	DB 5;	Length 889;
Best Local Similarity	49.9%;	Pred. No. 6.5e-25;		
Matches 381;	Conservative 1;	Mismatches 376;	Indels 6;	Gaps 1;
Qy	1	atgttaaactctgaaacaaacatatgtcatcatcgtgggaatcgcctaataaagcgtagttatt	60	
Db	16	atgggatttttaaaaggtaaaaaagggcttattgtagggtggggaacaataaattccatc	75	
Qy	61	gcttttggctgcgtaaagtttttagatcaaataggctgctaaattagattttacitacogt	120	
Db	76	gcttaagggaicgcgtcaatctgtttcaatcaaggggctacttttgctttccactatttg	135	
Qy	121	aaagaacgtagcgttaaagagcttgaaataattatgagacaattaaaaccaaccagaagcg	180	
Db	136	aatgagagtttagaaaagcggtaaggcctatcgcgcgaaggaattgaaatagccctatg--	193	
Qy	181	cacttatataaattgattgttcaagcgcgatgaagaggtttataatgggtttttgagcaaat	240	
Db	194	---tgatatgaattggatgtgagcaaaagagcattttcaagtgcgtatacaatagcggt	249	
Qy	241	ggtaaaagatgttgcaatatgtgatgtggtgtatatacttaattcgaatttgcgtaatatgaa	300	
Db	250	aaaaagggattaggctcatctatggattttatttttcaatagcgtggcctttgccttcaaacag	309	

Qy	301	gacttacgcggagcgcctttcttgaaacttccacgtgaaggctctctgttgaactcaagaacatt	360
Db	310	gctttagaggggagctgtgttggaactcttaaaagcgcgtttaacaccgcgtatggaatt	369
Qy	361	agttctactcattaaacaatttggctcatgaagctaaaaaaataatgccaagaagtgtt	420
Db	370	tctgtttattctttaatagagctgacaaacaccctaaaaccttta tgaatacggagcg	429
Qy	421	agcatttgttcaacaacacatatttaggtggcggaattcgcagttccaaaattataatgtgatg	480
Db	430	tctgttttgaactctaaactatttgggtagcaccaaaatacatgcgcattacaatgtgatg	489
Qy	481	gggtttgctaaagcgcgacttagaagcaaaatgttaaatatttagacattagacttagctct	540
Db	490	gggttggctaaagcgccttagagagtgcggtgcgtttatttagcgttggtatttaggcaaa	549
Qy	541	gataatttcgcgttaatgcaatttcagctgttccaatccgtacattaaagtgcaaaagt	600
Db	550	caccataaagagtgaatgccctatcgcgcggcctatttaggaacgtcgtcttagcggg	609
Qy	601	gtgggtgttttccaatcaaatctttaagaagaatcgaagagcgtgcacctttaaaacgtaac	660
Db	610	atcgcgtattttagaatgattttaaaaatggaatgaaatcaacgccctttaagaaaaaat	669
Qy	661	gttgatcaagtagaagtaggtataaacacgcggcttactttrttaagtgaacttacaagtgcg	720
Db	670	gtgagtttagaagaagtgggcaatgcgcggatgatttgcgtctagtgttgccttagcggg	729
Qy	721	gttacagggtaaaaatatctcatgtagatagcggattccacgcaat	764
Db	730	gtgagtggggaagtgcattttgttgatgctggtcatcatgttat	773

RESULT 12
 US-60-360-039-44878
 ; Sequence 44878, Application US/603600039
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF IMPROVED PROPERTIES
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)A
 ; CURRENT APPLICATION NUMBER: US/60/360,039
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 44878
 ; LENGTH: 786
 ; TYPE: DNA
 ; ORGANISM: Xenorhabdus nematophilus
 US-60-360-039-44878

	Query Match	17.9%	Score 137.8	DB 8	Length 786
	Best Local Similarity	51.2%	Pred. No. 2.2e-24		
	Matches 375	Conservative 1	Mismatches 348	Indels 9	Gaps 2
Qy	27	tgtcatcatgggaatcgctaaagcgtagtagtattgcgttttttggtatcgctaaagattttaga	86		
Db	27	tctcaattactggcgtagcgcgaactgtctatcgcttatgtaattgccaggccaatgca	86		
Qy	87	tcaattaggtctaaattagttatttacttaccgttaagaaacgctgacgctaaagagcttga	146		
Db	87	cgatcaaggagctgagctggcttttacctaccgaagaatgacaagttaaactctgctga	146		
Qy	147	aaaattattagacaacattaatcaaccgaagcgcaacttatatcaaatgttgattctcaag	206		
Db	147	agaattcgcgcgcattctggat-----tcgaacatcatcttgcgcattgtgatggctga	200		
Ov	207	cgatgaagagcttattagatgttttgacgaatttgataagcatattgacatattgata	266		

Db 201 agatgaagattatgacgcattattcgtgaactaggtgaagattatgacgctaaagttagcgg 260
Qy 267 tgaatacatcaatcgcatttgcataatgaagacttagcgcgacgtcttcttga 323
Db 261 ctgttgaactatattgttgcctcctgtgacagcgttgcaggtgattgattgaa 320
Qy 324 aactcagtgaaagcctctctgttagctcaagacattagttcttactcaataaattgt 383
Db 321 cgtcaacgtgaaggtttcaaaattgcacatgatcatcagtcacacgcttcgtcgtat 380
Qy 384 ggcctcatgaactaaaattaatgcagaaggtggtgagcattgttgcaacaacatattt 443
Db 381 ggcgaataatcatgcgcgaacatgttgaaatcctaactcagccctctcactcgtgactat 440
Qy 444 aggtggcaattcgcagttcaaaattataatgtaattggttgccttaaaagcgccttaga 503
Db 441 ggggtgcagacgtgcgaaccccttaatacaacgttaattggttgcgaagcttctcgtga 500
Qy 504 agcaaatgttaaatattagcattagacttagctcctgataatattcgcgttaattgcaat 563
Db 501 agctaaactgcgttatatgcgaatgcaatggtgctgaaggtgttcgtgtaacggtat 560
Qy 564 ttcagctggtccaatccgataatgaatgaaggtgcgaaggtggtggttccatacaattct 623
Db 561 ctccgcagggcccaattcgtacactggcagcatcggcactcaaaagatttccgcaagatgct 620
Qy 624 taagaaatcgaagagcgtgcaccttttaaaacgttaacgttgcataaagatttccgcaagatgct 683
Db 621 ggcacactgcgaagcgttaacactattcgcgtactgtaacaacagaagatgtaggttaa 680
Qy 684 aacagcggcttacttrttaagtgacttatcaagtggcgttacaggtgaaataattcattgt 743
Db 681 tgcagcagctcctgtgttctgacttctgctggtggtgacagggcaaaattatgcattgt 740
Qy 744 agatagcggattc 756
Db 741 cgtatggcgggtctc 753

RESULT 13

US-60-360-039-43253
; Sequence 43253, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 43253
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Nitrosomonas europaea
US-60-360-039-43253

Query Match 17.3%; Score 133; DB 8; Length 768;
Best Local Similarity 51.1%; Pred. No. 3.3e-23;
Matches 394; Conservative 0; Mismatches 365; Indels 12; Gaps 3;

Qy 1 atgttaactcttgaaacaaacataatgtcatcattggaatcgctaaataagcgtattt 60
Db 1 atgggattcttcggcggcggcaaatctgtattacgggctgtcagtaaccgctctatc 60
Qy 61 gcttttggtgcgtaaagttttagatacaattaggtgtcaaatagattagttactaccgt 120
Db 61 gcttacggtattgccaaagcaatgcagcgtgaagggcccaactggcattcacttaccag 120

Qy 121 aaagaacgtagccgtaaagagcttgaaaaattatttagaacaattaaatcaaccagaagcg 180
Db 121 tcgcatgatttacgcgagcgcacatcagtaaatagctgcagaattcaacagt-----gac 174
Qy 181 cacttatcatcaaatgatgttcaagcgatgaagaggttataatgggttttgagcaaat 240
Db 175 ctgctgttccgctgtgctcagtcagcagatgaagaaatcagccgttcttcagcgagctg 234
Qy 241 ggtaaagatgttgcaaatattgatgggtgtatatcatcattcaatcgcaatttgcataatggaa 300
Db 235 gcagatcactgggatggatggacggaatcgtacactccattgctcttgcaccgcgcaca 294
Qy 301 gacttaagcggcagcgttttctgaaacttca---cgtgaagcgtctctgttagctcaagac 357
Db 295 gcttgccggcgattattctggaagtgctgcagcagggcttttcattatgcacacgac 354
Qy 358 attagttcttactcattacaattgtggtcctcatgaagctaaaaaattaaatccaggaag- 416
Db 355 atcagctcatatagctttgccgcgtggcaaaagccgactgccactgatcgagggaag 414
Qy 417 --tggtagcattgttgcacaacataatttagttggcgaaattcgcagttcctcaaatataat 474
Db 415 ccgctcgtctcgtgcacactcagctatctcgttgcgtgacgtgtgatgccagctacaat 474
Qy 475 gtgatgggtgttgctaaagcagcttagaagcaaatgtttaaataatttagcattagactta 534
Db 475 gtgatgggtgttgccaaagccagcctggagggcaatgttctgtttatgcacagcctt 534
Qy 535 ggtcctgataatctcgcgttaattgcattcagctcagctcagctcagctcagctcagctc 594
Db 535 ggtaaacagggatcaggggtcaatgcaatttcagcttggaaccaatcaaacgcctgcgcga 594
Qy 595 aaaggtgtggtgttcaatacattcttaagaaatcgaagaaatcgaagcgtgcaccccttaaaa 654
Db 595 gcaggaatcggcaattttgcaaaactcgtgggacattctgtaaaagtttcgctcctgaaa 654
Qy 655 cgtaacgttgcataagtagtagtaaaacagcgcgttacttrttaagtgcattatca 714
Db 655 cgaacgtgaccactgaagatcggtgaatgtagcgcttcttcttgcagtgatcgtgcc 714
Qy 715 agtggcgttacagcgtgaaataattcattcagtagatagcggattccacgcaatt 785
Db 715 agtggatcactggtgaaatcacttatgtggtgagtcgggattcaataacgtt 765

RESULT 14

US-60-360-039-35437
; Sequence 35437, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35437
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-60-360-039-35437

Query Match 16.8%; Score 129.2; DB 8; Length 783;
Best Local Similarity 50.3%; Pred. No. 2.9e-22;
Matches 370; Conservative 1; Mismatches 359; Indels 6; Gaps 2;
Qy 29 tcatcatcgggaatcgcgttaataagcgtagtagttgcttttgggtgcgtctaaagttagatc 88

```

Db 26 tcacatggtggtcgccataaacggttcaatcgcttggggcattgcaaaagggcgtgcg 85
Qy 89 aattaggtgtctaaatttagttatttacttaccgttaaaagacgtagccgttaaaagagcttgaaa 148
Db 86 atgcaggtgcggaacgtcacctcacctgcaggggtg-acgcattgaagaagcgcgtcgag 144
Qy 149 aattattagaacaataataatcaaccagaagcgcacattatatacaaatgtatgttcaaaagcg 208
Db 145 cctctcgccaggaactgcgctttcattggcggccattgcagctgacgtaccgacatctcgag 204
Qy 209 atgaagaggttattaatgttttgagcaaatgttgaagatgttgcaatatattgattgggtg 268
Db 205 acga-----tcgactccgttttgcctgcctggaaacagcattggggcgaagatcgacttcg 259
Qy 269 tatattcattcaactgcatttgcataatggaagacttaacgcgcacgtctttcttgaacatt 328
Db 260 tctgtcacgccattgcgttctcgcacaaagacgagctgaccggccgtttatctcgtatacca 319
Qy 329 cactggaaggtctctgttagctcaagacattagtttcttactcattatacaaatgttggtc 388
Db 320 gcgcgacaaacttcaaccgcacattggtatattccgtgttctcgtgcgcgcgtttgcaa 379
Qy 389 atgaagctaaaaataatgcccagaaggtgtagcattgttgcaacaacatatattaggtg 448
Db 380 agcgcagagcccatcgatgaatgacggcgttgcacatcacgcgttacctattacggcg 439
Qy 449 gcgaattcgcagttcaaaattataatgtaggggtgtgtctaaagcgagcttagaagcaa 508
Db 440 ccgaagaaggtcagcggaattacaacgtgagggcgtggccaaagcgcgtcttgaagcca 499
Qy 509 atgttaaatatttagcattagacttagctgactgataatattcgcgttaataatgcaatttcag 568
Db 500 gcgtgcttattcgcgcgtgcacgtcgtgtaacgcggcattccgcgtcaacgcgcgtttccg 559
Qy 569 ctggtccaatccgtacataaagtgcaaaaggtgtggtgtgttccaatatacaattcttaag 628
Db 560 ccggcccgatcaagacgcttgcgggttcggcgtacgcgtggttccgttaccattctgaagt 619
Qy 629 aatcgaagagcgtgcaccttttaaaacgttaacgttgcattgaagtagaagtaggttaaaacag 688
Db 620 ggaacgaataatgcgcgtgaaagcgcacgttaccatcgaggaagtcggcaagtcgg 679
Qy 689 cggcttacttrttaagtgaacttcaaggtggcgttacaggtgaaaaattatcattgtagata 748
Db 680 cgtctacotgtgttcgcgacctttcgacggtgacggcgtgacccgtggaatccaccattcgatt 739
Qy 749 gcggattccacgcaat 764
Db 740 ccggctatcacaccat 755

```

RESULT 15
 US-60-039-37978
 ; Sequence 37978, Application US/60360039
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)A
 ; CURRENT APPLICATION NUMBER: US/60/360,039
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 37978
 ; LENGTH: 783
 ; TYPE: DNA
 ; ORGANISM: Agrobacterium tumefaciens
 US-60-360-039-37978

```

Query Match 16.8%; Score 129.2; DB 8; Length 783;
Best Local Similarity 50.3%; Pred. No. 2.9e-22;
Matches 370; Conservative 1; Mismatches 359; Indels 6; Gaps 2;

Qy 29 tcacatggtggtcgccataaacggttcaatcgcttggggcattgcaaaagggcgttcgatac 88
Db 26 tcacatggtggtcgccataaacggttcaatcgcttggggcattgcaaaagggcgttcgatac 85
Qy 89 aattaggtgtctaaatttagttatttacttaccgttaaaagacgtagccgttaaaagagcttgaaa 148
Db 86 atgcaggtgcggaacgtcacctcacctgcaggggtg-acgcattgaagaagcgcgtcgag 144
Qy 149 aattattagaacaataataatcaaccagaagcgcacattatatacaaatgtatgttcaaaagcg 208
Db 145 cctctcgccaggaactgcgctttcattggcggccattgcagctgacgtaccgacatctcgag 204
Qy 209 atgaagaggttattaatgttttgagcaaatgttgaagatgttgcaatatattgattgggtg 268
Db 205 acga-----tcgactccgttttgcctgcctggaaacagcattggggcgaagatcgacttcg 259
Qy 269 tatattcattcaactgcatttgcataatggaagacttaacgcgcacgtctttcttgaacatt 328
Db 260 tctgtcacgccattgcgttctcgcacaaagacgagctgaccggccgtttatctcgtatacca 319
Qy 329 cactggaaggtctctgttagctcaagacattagtttcttactcattatacaaatgttggtc 388
Db 320 gcgcgacaaacttcaaccgcacattggtatattccgtgttctcgtgcgcgcgtttgcaa 379
Qy 389 atgaagctaaaaataatgcccagaaggtgtagcattgttgcaacaacatatattaggtg 448
Db 380 agcgcagagcccatcgatgaatgacggcgttgcacatcacgcgttacctattacggcg 439
Qy 449 gcgaattcgcagttcaaaattataatgtaggggtgtgtctaaagcgagcttagaagcaa 508
Db 440 ccgaagaaggtcagcggaattacaacgtgagggcgtggccaaagcgcgtcttgaagcca 499
Qy 509 atgttaaatatttagcattagacttagctgactgataatattcgcgttaataatgcaatttcag 568
Db 500 gcgtgcttattcgcgcgtgcacgtcgtgtaacgcggcattccgcgtcaacgcgcgtttccg 559
Qy 569 ctggtccaatccgtacataaagtgcaaaaggtgtggtgtgttccaatatacaattcttaag 628
Db 560 ccggcccgatcaagacgcttgcgggttcggcgtacgcgtggttccgttaccattctgaagt 619
Qy 629 aatcgaagagcgtgcaccttttaaaacgttaacgttgcattgaagtagaagtaggttaaaacag 688
Db 620 ggaacgaataatgcgcgtgaaagcgcacgttaccatcgaggaagtcggcaagtcgg 679
Qy 689 cggcttacttrttaagtgaacttcaaggtggcgttacaggtgaaaaattatcattgtagata 748
Db 680 cgtctacotgtgttcgcgacctttcgacggtgacggcgtgacccgtggaatccaccattcgatt 739
Qy 749 gcggattccacgcaat 764
Db 740 ccggctatcacaccat 755

```

Search completed: September 22, 2002, 16:59:29
 Job time: 4310 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 16:00:24 ; Search time 24.87 seconds
(without alignments)
251.425 Million cell updates/sec

Title: US-09-292-411A-2
Perfect score: 1277
Sequence: 1 MLNLENTYVINGTANKRSI.....LSSGVGTGNIHVDGPFHAIK 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2.6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2.6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2.6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2.6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2.6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2.6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	542.5	42.5	262	1 US-08-241-766-9	Sequence 9, Appli
2	529.5	41.5	262	1 US-08-241-766-8	Sequence 8, Appli
3	322.5	25.3	390	4 US-09-586-719-2	Sequence 2, Appli
4	295.5	23.1	269	1 US-08-241-766-6	Sequence 6, Appli
5	292.5	22.9	269	1 US-08-241-766-7	Sequence 7, Appli
6	280.5	22.0	269	1 US-08-241-766-4	Sequence 4, Appli
7	278.5	21.8	269	1 US-08-241-766-5	Sequence 5, Appli
8	278.5	21.8	269	1 US-08-241-766-14	Sequence 14, Appli
9	190.5	14.9	262	4 US-09-363-189B-6	Sequence 6, Appli
10	179.5	14.1	292	3 US-09-109-205-2	Sequence 2, Appli
11	172	13.5	244	1 US-08-762-129-4	Sequence 4, Appli
12	171	13.4	244	1 US-08-762-129-3	Sequence 3, Appli
13	170	13.3	244	1 US-08-762-129-1	Sequence 1, Appli
14	169	13.2	295	3 US-09-002-298-5	Sequence 5, Appli
15	166	13.0	244	2 US-09-090-567-2	Sequence 2, Appli
16	165.5	13.0	255	4 US-08-815-225-4	Sequence 4, Appli
17	163	12.8	335	3 US-09-002-298-6	Sequence 6, Appli
18	157	12.3	335	3 US-09-109-205-19	Sequence 19, Appli
19	155.5	12.2	283	4 US-09-367-012-1	Sequence 1, Appli
20	153.5	12.0	303	3 US-09-002-298-1	Sequence 1, Appli
21	150	11.7	244	1 US-08-375-962B-13	Sequence 13, Appli
22	150	11.7	244	2 US-08-562-114B-13	Sequence 13, Appli
23	150	11.7	244	4 US-08-729-594A-13	Sequence 13, Appli
24	138	10.8	335	3 US-09-002-298-7	Sequence 7, Appli
25	131.5	10.3	256	1 US-08-594-808B-7	Sequence 7, Appli
26	126	9.9	246	3 US-09-238-481-2	Sequence 2, Appli
27	125.5	9.8	313	4 US-09-413-814-9	Sequence 9, Appli

28	124.5	9.7	231	2	US-08-336-198C-7	Sequence 7, Appli
29	123.5	9.7	261	4	US-09-468-738A-29	Sequence 29, Appli
30	121	9.5	243	4	US-09-239-052-2	Sequence 2, Appli
31	120.5	9.4	388	4	US-08-980-832-41	Sequence 41, Appli
32	120	9.4	246	6	5229279-7	Patent No. 5229279
33	119	9.3	333	1	US-08-440-856A-4	Sequence 4, Appli
34	112	8.8	247	1	US-08-241-766-13	Sequence 13, Appli
35	111	8.7	292	4	US-09-468-738A-2	Sequence 2, Appli
36	111	8.7	296	4	US-09-468-738A-23	Sequence 23, Appli
37	111	8.7	337	1	US-08-440-856A-3	Sequence 3, Appli
38	108	8.5	323	2	US-09-019-216-3	Sequence 3, Appli
39	106.5	8.3	315	3	US-08-793-035-9	Sequence 9, Appli
40	106.5	8.3	315	3	US-08-793-035-10	Sequence 10, Appli
41	106	8.3	186	4	US-08-858-207A-270	Sequence 270, App
42	105	8.2	252	3	US-08-822-322-8	Sequence 8, Appli
43	105	8.2	252	4	US-09-466-109-8	Sequence 8, Appli
44	104.5	8.2	257	4	US-09-287-097-2	Sequence 2, Appli
45	103.5	8.1	271	2	US-07-637-865-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-241-766-9
; Sequence 9, Application US/08241766
; Patent No. 5686590
; GENERAL INFORMATION:
; APPLICANT: JACOBS, W. R.
; APPLICANT: COLLINS, D. M.
; APPLICANT: BANERJEE, A.
; APPLICANT: DELISLE, G. W.
; APPLICANT: WILSON, T. M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN INHA AGENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,766
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, GLADYS H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 25237-20003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 262 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-241-766-9

Query Match 42.5% Score 542.5; DB 1; Length 262;
Best Local Similarity 44.0%; Pred. No. 2.6e-46;
Matches 110; Conservative 52; Mismatches 85; Indels 3; Gaps 2;

; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US/08/241,766
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, GLADYS H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 25237-20003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-241-766-14

Query Match 21.8%; Score 278.5; DB 1; Length 269;
Best Local Similarity 31.4%; Pred. No. 5.8e-20;
Matches 86; Conservative 57; Mismatches 94; Indels 37; Gaps 11;
QY 4 LENKTVIMGINKRSTAFQVAKVLDQLGAKLVFTYRKRSRKELEKLEQLNQPEAHLY 63
Db 5 LDGKRILVSGIITDSIAFHIAVQEQAGQLVLT-GFDELRL-IQRTDRL-PAPAPLL 61
QY 64 QIDVQDEEVINGFEIQKDVG---NIDGVYHSIAFANMEDL-----RGFSETSGREGF 114
Db 62 ELDVQNEEHLASLAGRVTAIGAGNKLGVVHAIGFMPQTMGMINPFDPAPYADVSK--- 118
QY 115 LLAQDISSYSLTVAHEAKKLMPGEGSIVATYTLGGEF---AVQYNYMGVAKASLEAN 170
Db 119 --GIHSAYSASYAMAKALLPIMPGGISV-----GMDFFDSRAMPAYNNMTVAKSALESV 171
QY 171 VKYALDLGPDNIRVNAISAGPRTISAKGV-----GGFNTILKE-IEERAPLKN 220
Db 172 NRVAREAGKYGVRSNLVRAAGPRTILAMSAIVGALGEEAGAGIQLLEGGWDQRAPIGWN 231
QY 221 V-DOVEVGKTAAYLLSDLSGGVTGENIHVDSPGH 253
Db 232 MKDATPVAKTVCALLSDWLPATTTGDIYADGGAH 265

RESULT 9
US-09-363-1898-6
; Sequence 6, Application US/093631898
; Patent No. 6242228
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZAKI, KENZO
; TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/09/363,189B
; CURRENT FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6

; LENGTH: 262
; TYPE: PRT
; ORGANISM: Gluconobacter oxydans
; US-09-363-1898-6
Query Match 14.9%; Score 190.5; DB 4; Length 262;
Best Local Similarity 29.6%; Pred. No. 3.4e-11;
Matches 68; Conservative 41; Mismatches 96; Indels 25; Gaps 7;
QY 42 ERSRKELEKLEQLNOP--EAHLYQIDVQDEEVINGFEIQKDVGNIDGVYHSI-----A 95
Db 38 DMNREALEKAEASVREKGVARSYVCDVTSEAVIGTVDSVVRDFGKIDFLFNAGYQGA 97
QY 96 FANMEDLRGRFSETSGREGFLLAQDISSYSLTVAHEAKKLMPGEGSIVATYTLGGEFAVQ 155
Db 98 FAPVQDYPSS--DDFAR---VLTINVTGAFHVLKAVSRQMITQNYGRIVNTASMAVKGPP 152
QY 156 NYNMGVAKASLEANVYKYLALDGLPDNIRVNAISAGPRTISAKGVGSGFN 205
Db 153 NMAAYGASKGAIILATETAALDLAPYINRVNAISPGYMGPGFMWEROVELQAKVGSQYFS 212
QY 206 TILKEIEER---APLKRNVDOVEVGKTAAYLLSDLSGGVTGENIHVDSDG 251
Db 213 TDPKVVAQQMIGSVPHRRYGDINEIPGVVAFLLGDDSSFTMTGVNLPATGG 262

RESULT 10
US-09-109-205-2
; Sequence 2, Application US/09109205
; Patent No. 6057140
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Gorgone, Gina
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,205
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0542 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-855-0572
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: PROSTUT12
CLONE: 1810320
US-09-109-205-2

Query Match 14.1%; Score 179.5; DB 3; Length 292;
Best Local Similarity 29.3%; Pred. No. 5e-10;
Matches 76; Conservative 42; Mismatches 116; Indels 25; Gaps 11;
QY 4 LENKTVIMGIANKRSIAFGVAKVLDOLGAKLVFTYRK-ERSRKELEKLEQLNQPEAHL 62
DB 26 LDKVAFITG--GGSGIGFRIAEIFMRHGCHTVIASRSLPRLVLTAAKLAGATGRCLPL 83
QY 63 YQIDVQSDDEVINGFEQIGKDVGNIDGVVHSTAFANMEDLRGF-----SETSRGFFLLAQ 118
DB 84 -SMDVRAPPVNAVDQALKEFRIDILNCAA-----GNFLCPAGALSFNFAKTVM 134
QY 119 DI---SSYSLTIVAHEAKKLMEGGSIV-ATTYLGGE-FAVONYNVMGVAKASLEANYKY 173
DB 135 DIDTSGTFNVSRVLYE-KFFRDHGGVIVNITATLGNRQALQVH--AGSAAAVDAMTRH 191
QY 174 LALDGLPONIRVNAISAGPIR-TLSAKGVGGFNTILKEERAPLKRNVDOVEVGKTAAY 232
DB 192 LAVENGPNIRVNSLAPGISGELRRLLGGPQASLSTKVTASPLRLGNKTEIAHSVLY 251
QY 233 LLSLSSGVTGENIHVDSG 251
DB 252 LASPLASYVTGAVLVADGG 270

RESULT 11
US-08-762-129-4
Sequence 4, Application US/08762129
Patent No. 5756299
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN CARBONYL REDUCTASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,129
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0171 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 50004
US-08-762-129-4

Query Match 13.5%; Score 172; DB 1; Length 244;
Best Local Similarity 24.5%; Pred. No. 2.1e-09;
Matches 63; Conservative 53; Mismatches 121; Indels 20; Gaps 7;
QY 2 LNLNKTVIMGIANKRSIAFGVAKVLDOLGAKLVFTYRKRSRKELEKLEQLNQPEAHL 61
DB 3 LNFSGRLALVTGAG--KGIGRDTVKALHASGAKVYAV---TRTNSDLVSLAKECPGIEPV 57
QY 62 LYQI-DVOSDEIVINGFEQIGKDVGNIDGVVHSTAFANMEDLRGFSETSRGFFLLAODI 120
DB 58 CVDIGDWDATKALGG-----IGVDLLVNNAALVIMQP-----FLEVTREAFDRSPSV 106
QY 121 SSYSLTIVAH-EAKKLMEG--GSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALD 177
DB 107 NLRSVFQVSQVARDMINRGVPGSIVNVYSSMVAHVTFEPNLITYSSTKGAMTMTKAMAME 166
QY 178 LQPDNIRVNAISAGPIRLSAKGVCGFNTILKEERAPLKRNVDOVEVGKTAAYLLSOL 237
DB 167 LGPHKIRVNSNPTVYVLTDMGKVSADPEFARKLKRHLRKFARFEDVNVNSILFLSDR 226
QY 238 SSGVTGENIHVDSGFHA 254
DB 227 SASISGGGILVDAGYLA 243

RESULT 12
US-08-762-129-3
Sequence 3, Application US/08762129
Patent No. 5756299
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN CARBONYL REDUCTASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,129
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0171 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 416425
US-08-762-129-3

Query Match 13.4%; Score 171; DB 1; Length 244;
Best Local Similarity 24.1%; Pred. No. 2.7e-09;
Matches 58; Conservative 57; Mismatches 108; Indels 18; Gaps 6;
QY 18 RSTAFGAKVLDQGLAKLVFTYRKRSRKELEKLLQALNOPEAHLYQI-DVQSDDEEVING 76
DB 17 KGIGRVTVALHVSARGAVAV---TTNGDLVSLSQECGIEPCVVDLGDWEATERALGG 73
QY 77 FEOIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGEFLLAQDISYSITIVAH-EAKKL 135
DB 74 -----VGPVDLLVNNAAVALMQP---FLDTTKEVDFORSFVNLRSVQVSOIVARSM 122
QY 136 MPFG--GSIVATYTLGGEFAVQNYVMGVAKASLEANNVYKYLALDLPDNIIRVNAISAGPI 193
DB 123 IERGVPGSIVNVSMSVSHVTYTPGLAAYSTKGAMTMTKSMAMELGPHKLRVNSVNPVTVV 182
QY 194 RTLSAKGVGCFNTILKEIERAPLKRNVQVEVGKTAAYLLSDLSGGVTGENIHVDSGGFH 253
DB 183 LTAMGRSVTSDPELARKLKRHPMRKFAEVEDVNSILFLSDRSASTSGSIFVDAGYL 242
QY 254 A 254
DB 243 A 243

RESULT 13
US-08-762-129-1
Sequence 1, Application US/08762129
Patent No. 5756299
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN CARBONYL REDUCTASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,129
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0171 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
US-08-762-129-1

Query Match 13.3%; Score 170; DB 1; Length 244;
Best Local Similarity 24.9%; Pred. No. 3.4e-09;
Matches 64; Conservative 53; Mismatches 120; Indels 20; Gaps 7;
QY 2 LNLNKTYVIMGTIANRSTAFGVAKVLDQGLAKLVFTYRKRSRKELEKLLQALNOPEAH 61
DB 3 LFTAGRLVLTGAG--KGIGRVTVALHATGARVAV---SRTQADLSDSLVRECPGLEPV 57
QY 62 LYQI-DVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGEFLLAQDI 120
DB 58 CVDLGDWEATERALG-----SVGPVDLLVNNAAVALMQP---FLEVTKEAFDRSFV 106
QY 121 SSVSLTIVAH-EAKKLMPFG--GSIVATYTLGGEFAVQNYVMGVAKASLEANNVYKYLALD 177
DB 107 NLRAVIQVSOIVARGLIARGVPGAIIVNVSSQCSQRAVTNHSVYCSKTKGALDMLTKVNALE 166
QY 178 LGPDNIIRVNAISAGPIRTLSAKGVGCFNTILKEIERAPLKRNVQVEVGKTAAYLLSDL 237
DB 167 LGPHKLRVNAVNTVVTWSMGQATWSDPHKAKTXNRPXGKFAEVEHHVNNAILFLLSDR 226
QY 238 SSGVTGENIHVDSGFHA 254
DB 227 SGMTTGSTLPVEGGFWA 243

RESULT 14
US-09-002-298-5
Sequence 5, Application US/09002298
Patent No. 6046001
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Tang, Y. Tom
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN FATTY ACID BETA-OXIDATION ENZYMES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,298
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0453 US
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid

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OM protein - protein search, using sw model

Run on: September 22, 2002, 16:05:59 ; Search time 182.74 Seconds
(without alignments)
493.089 Million cell updates/sec

Title: US-09-292-411a-2
Perfect score: 1277
Sequence: 1 MLNLENTYIMGIANKRSI.....LSSGVTGENIHVDSGFHAIK 256

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Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
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15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
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19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
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21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
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25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1277	100.0	256	1	PCT-US02-03987-5228
3	1277	100.0	256	1	PCT-US02-03987-12535
4	1277	100.0	256	1	PCT-US02-03987-12892
5	1277	100.0	256	11	US-08-790-043A-1
6	1277	100.0	256	11	US-08-790-043A-1
7	1277	100.0	256	11	US-08-790-043B-2

8	1277	100.0	256	16	US-09-292-411-2	Sequence 2, Appli
9	1277	100.0	256	16	US-09-292-411A-2	Sequence 2, Appli
10	1277	100.0	256	16	US-09-292-412-2	Sequence 2, Appli
11	1277	100.0	256	22	US-09-815-242-5228	Sequence 5228, Ap
12	1277	100.0	256	22	US-09-815-242-12535	Sequence 12535, A
13	1277	100.0	256	22	US-09-815-242-12892	Sequence 12892, A
14	1277	100.0	256	24	US-10-009-219-2	Sequence 2, Appli
15	1277	100.0	256	24	US-10-072-851-5228	Sequence 5228, Ap
16	1277	100.0	256	24	US-10-072-851-12535	Sequence 12535, A
17	1277	100.0	256	24	US-10-072-851-12892	Sequence 12892, A
18	1277	100.0	256	26	US-60-242-578-690	Sequence 690, App
19	1277	100.0	256	26	US-60-253-625-2034	Sequence 2034, Ap
20	1277	100.0	256	26	US-60-257-931-2740	Sequence 2740, Ap
21	1277	100.0	256	26	US-60-269-308-3759	Sequence 3759, Ap
22	1271	99.5	256	1	PCT-US99-19726-6	Sequence 6, Appli
23	1271	99.5	256	19	US-09-512-255-6	Sequence 12, Appli
24	1263	98.9	255	1	PCT-US00-29451-12	Sequence 16, Appli
25	1225.5	96.0	263	16	US-09-266-555-16	Sequence 3776, Ap
26	1225.5	96.0	264	20	US-09-611-529-3776	Sequence 4009, Ap
27	1198	93.8	260	15	US-09-134-001C-4009	Sequence 5816, Ap
28	1198	93.8	260	18	US-09-450-969-5816	Sequence 6, Appli
29	1156	90.5	256	19	US-09-512-255A-6	Sequence 559, App
30	780	61.1	194	1	PCT-US97-02318-559	Sequence 559, App
31	780	61.1	194	13	US-08-903-470-559	Sequence 10515, A
32	623	48.8	250	1	PCT-US02-03987-10515	Sequence 10515, A
33	623	48.8	250	22	US-09-815-242-10515	Sequence 10515, A
34	623	48.8	250	24	US-10-072-851-10515	Sequence 9038, Ap
35	591	46.3	272	21	US-09-739-449-9038	Sequence 8211, Ap
36	591	46.3	272	22	US-09-803-110-9038	Sequence 11302, A
37	559	43.8	303	17	US-09-328-352-8211	Sequence 11302, A
38	556	43.5	275	1	PCT-US02-03987-11302	Sequence 1228, Ap
39	556	43.5	275	13	PCT-US98-06371-1228	Sequence 494, App
40	556	43.5	275	13	US-08-902-615A-494	Sequence 11302, A
41	556	43.5	275	22	US-09-815-242-11302	Sequence 11302, A
42	556	43.5	275	24	US-10-072-851-11302	Sequence 7, Appli
43	551	43.1	268	18	US-09-438-144-7	Sequence 4697, Ap
44	548.5	43.0	275	19	US-09-543-681A-4697	Sequence 24, Appli
45	542.5	42.5	262	1	PCT-US00-29451-24	

ALIGNMENTS

RESULT 1
PCT-US00-12104-2
; Sequence 2, Application PC/TUS0012104
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM plc
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS
; FILE REFERENCE: GM50056
; CURRENT APPLICATION NUMBER: PCT/US00/12104
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/134,362
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
PCT-US00-12104-2

Query Match 100.0%; Score 1277; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLNLENTYIMGIANKRSIAGVAKVLDQLGAKLVFTYRKRSRKEKLEQLNOPEA 60
DB 1 MLNLENTYIMGIANKRSIAGVAKVLDQLGAKLVFTYRKRSRKEKLEQLNOPEA 60

```
Qy 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
Db 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
Qy 121 SSYSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLLALDLGP 180
Db 121 SSYSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLLALDLGP 180
Qy 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSGG 240
Db 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSGG 240
Qy 241 VTGENIHVDSGFHAIK 256
Db 241 VTGENIHVDSGFHAIK 256

RESULT 2
PCT-US02-03987-5228
; Sequence 5228, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elittra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5228
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
PCT-US02-03987-5228
```

```
Query Match 100.0%; Score 1277; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKEKLEQLNQPEA 60
Db 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKEKLEQLNQPEA 60
Qy 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
Db 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
Qy 121 SSYSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLLALDLGP 180
Db 121 SSYSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLLALDLGP 180
Qy 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSGG 240
Db 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSGG 240
Qy 241 VTGENIHVDSGFHAIK 256
Db 241 VTGENIHVDSGFHAIK 256

RESULT 3
PCT-US02-03987-12535
; Sequence 12535, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elittra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
```

```
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12535
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
PCT-US02-03987-12535
```

```
Query Match 100.0%; Score 1277; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKEKLEQLNQPEA 60
Db 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKEKLEQLNQPEA 60
Qy 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
Db 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
Qy 121 SSYSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLLALDLGP 180
Db 121 SSYSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLLALDLGP 180
Qy 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSGG 240
Db 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSGG 240
Qy 241 VTGENIHVDSGFHAIK 256
Db 241 VTGENIHVDSGFHAIK 256
```

```
RESULT 4
PCT-US02-03987-12892
; Sequence 12892, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elittra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12892
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
PCT-US02-03987-12892
```

```
Query Match 100.0%; Score 1277; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKEKLEQLNQPEA 60
Db 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKEKLEQLNQPEA 60
Qy 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
Db 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
Qy 121 SSYSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLLALDLGP 180
Db 121 SSYSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLLALDLGP 180
```

QY 181 DNRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240
Db 181 DNRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240
QY 241 VTGENIHVDSGFHAIK 256
Db 241 VTGENIHVDSGFHAIK 256

RESULT 5

US-08-790-043-1
; Sequence 1, Application US/08790043
; GENERAL INFORMATION:
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: Novel Fabi
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,043
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024845
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: GM50005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-043-1

Query Match 100.0%; Score 1277; DB 11; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLNLENTVYIMGIANKRSIAFGVAKVLDOLGAKLVFTYRKRSRKELEKLLLEQLNQPEA 60
Db 1 MLNLENTVYIMGIANKRSIAFGVAKVLDOLGAKLVFTYRKRSRKELEKLLLEQLNQPEA 60
QY 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGYHSHAFANMEDLGRFSETSRGFLLAQDI 120
Db 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGYHSHAFANMEDLGRFSETSRGFLLAQDI 120
QY 121 SSVSLTIVAEAKKLMPEGGSIVATTYLGGEFAVQNYVMGVAKASLEANKVYLAIDLGP 180
Db 121 SSVSLTIVAEAKKLMPEGGSIVATTYLGGEFAVQNYVMGVAKASLEANKVYLAIDLGP 180
QY 181 DNRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240

Db 181 DNRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240
QY 241 VTGENIHVDSGFHAIK 256
Db 241 VTGENIHVDSGFHAIK 256

RESULT 6

US-08-790-043A-1
; Sequence 1, Application US/08790043A
; GENERAL INFORMATION:
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: Novel Fabi
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,043A
; FILING DATE: 28-August-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024845
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: GM50005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-043A-1

Query Match 100.0%; Score 1277; DB 11; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLNLENTVYIMGIANKRSIAFGVAKVLDOLGAKLVFTYRKRSRKELEKLLLEQLNQPEA 60
Db 1 MLNLENTVYIMGIANKRSIAFGVAKVLDOLGAKLVFTYRKRSRKELEKLLLEQLNQPEA 60
QY 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGYHSHAFANMEDLGRFSETSRGFLLAQDI 120
Db 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGYHSHAFANMEDLGRFSETSRGFLLAQDI 120
QY 121 SSVSLTIVAEAKKLMPEGGSIVATTYLGGEFAVQNYVMGVAKASLEANKVYLAIDLGP 180
Db 121 SSVSLTIVAEAKKLMPEGGSIVATTYLGGEFAVQNYVMGVAKASLEANKVYLAIDLGP 180
QY 181 DNRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240

Db 181 DNIIRVNAISAGPIRTLSAKGVGGENTILKEIERAPLKRNVQDVGVKTAAYLLDSSG 240

RESULT 7
US-08-790-043B-2

Query Match	100.0%	Score 1277;	DB 11;	Length 256;
Best Local Similarity	100.0%	Pred. No. 8.4e-118;		
Matches 256;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps				0;

QY 241 VTGENIHVDSGFHAIK 256
 |||||
 Db 241 VTGENIHVDSGFHAIK 256

RESULT 8
 US-09-292-411-2
 ; Sequence 2, Application US/09292411
 ; GENERAL INFORMATION:
 ; APPLICANT: Payne, David
 ; APPLICANT: Lonsdale, John
 ; APPLICANT: Milner, Peter
 ; APPLICANT: Pearson, Stewart
 ; TITLE OF INVENTION: FAB I
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 4000 Bell Atlantic Tower, 1717 Arch Street
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: US
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/292,411
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/790,043
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Falk, Stephen T
 ; REGISTRATION NUMBER: 36,795
 ; REFERENCE/DOCKET NUMBER: GM50005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-994-2488
 ; TELEFAX: 215-994-2222
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 256 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-292-411-2

```
Query Match      100.0%; Score 1277; DB 16; Length 256;
Best Local Similarity 100.0%; Pred. NO. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/292,412
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/790,043
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T.
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM50005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-292-412-2

Query Match          100.0%; Score 1277; DB 16; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 MLNLENTYYIMGIANKRSTAFGVAKVLDQLGAKLVFTYRKRSRKEKLEQLNQPEA 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1 MLNLENTYYIMGIANKRSTAFGVAKVLDQLGAKLVFTYRKRSRKEKLEQLNQPEA 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   61 HLYQIDVQSDEEVINGFEQIGKDVGNDGYVHSTAFANMEDLRGRFSETSGEFLAQDI 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   61 HLYQIDVQSDEEVINGFEQIGKDVGNDGYVHSTAFANMEDLRGRFSETSGEFLAQDI 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   121 SSVSLTIVAHEAKKLMPGGSIATTVLGCFAFVNVMGVAKASLEANYKYLLDGLGP 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   121 SSVSLTIVAHEAKKLMPGGSIATTVLGCFAFVNVMGVAKASLEANYKYLLDGLGP 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEERAPLKRNVDQVEVGKTAAYLLSDLSG 240
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEERAPLKRNVDQVEVGKTAAYLLSDLSG 240
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   241 VTGENIHVDSGFHAIK 256
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   241 VTGENIHVDSGFHAIK 256
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-09-815-242-5228
; Sequence 5228, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/292,412
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/790,043
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T.
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM50005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-292-412-2

Query Match          100.0%; Score 1277; DB 16; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 MLNLENTYYIMGIANKRSTAFGVAKVLDQLGAKLVFTYRKRSRKEKLEQLNQPEA 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1 MLNLENTYYIMGIANKRSTAFGVAKVLDQLGAKLVFTYRKRSRKEKLEQLNQPEA 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   61 HLYQIDVQSDEEVINGFEQIGKDVGNDGYVHSTAFANMEDLRGRFSETSGEFLAQDI 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   61 HLYQIDVQSDEEVINGFEQIGKDVGNDGYVHSTAFANMEDLRGRFSETSGEFLAQDI 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   121 SSVSLTIVAHEAKKLMPGGSIATTVLGCFAFVNVMGVAKASLEANYKYLLDGLGP 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   121 SSVSLTIVAHEAKKLMPGGSIATTVLGCFAFVNVMGVAKASLEANYKYLLDGLGP 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEERAPLKRNVDQVEVGKTAAYLLSDLSG 240
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEERAPLKRNVDQVEVGKTAAYLLSDLSG 240
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   241 VTGENIHVDSGFHAIK 256
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   241 VTGENIHVDSGFHAIK 256
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
US-09-292-412-2
; Sequence 2, Application US/09292412
; GENERAL INFORMATION:
; APPLICANT: Payne, David
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: Fab I
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5228
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5228

Query Match 100.0%; Score 1277; DB 22; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLNLENKTYIVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLEQLNQPEA 60
Db 1 MLNLENKTYIVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLEQLNQPEA 60
QY 61 HLYQIDVQSDDEEVINGFQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRGFLLAQDI 120
Db 61 HLYQIDVQSDDEEVINGFQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRGFLLAQDI 120
QY 121 SSYSLTIVAHAKKLMPGEGSIVATTYLGGEFAVQNYNMGVAKASLEANYKYIALDLGP 180
Db 121 SSYSLTIVAHAKKLMPGEGSIVATTYLGGEFAVQNYNMGVAKASLEANYKYIALDLGP 180
QY 181 DNIRVNAISAGPIRTLSAKGVGGNTILKEETEERAPLKRNVDOVEVGKTAAYLLSDLSG 240
Db 181 DNIRVNAISAGPIRTLSAKGVGGNTILKEETEERAPLKRNVDOVEVGKTAAYLLSDLSG 240
QY 241 VTGENIHVDSGFHAIK 256
Db 241 VTGENIHVDSGFHAIK 256

RESULT 12
US-09-815-242-12535
; Sequence 12535, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12535
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12535

Query Match 100.0%; Score 1277; DB 22; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLNLENKTYIVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLEQLNQPEA 60
Db 1 MLNLENKTYIVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLEQLNQPEA 60
QY 61 HLYQIDVQSDDEEVINGFQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRGFLLAQDI 120
Db 61 HLYQIDVQSDDEEVINGFQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRGFLLAQDI 120
QY 121 SSYSLTIVAHAKKLMPGEGSIVATTYLGGEFAVQNYNMGVAKASLEANYKYIALDLGP 180
Db 121 SSYSLTIVAHAKKLMPGEGSIVATTYLGGEFAVQNYNMGVAKASLEANYKYIALDLGP 180
QY 181 DNIRVNAISAGPIRTLSAKGVGGNTILKEETEERAPLKRNVDOVEVGKTAAYLLSDLSG 240
Db 181 DNIRVNAISAGPIRTLSAKGVGGNTILKEETEERAPLKRNVDOVEVGKTAAYLLSDLSG 240
QY 241 VTGENIHVDSGFHAIK 256
Db 241 VTGENIHVDSGFHAIK 256

RESULT 13
US-09-815-242-12892
; Sequence 12892, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12892
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12892

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Query Match      100.0%; Score 1277; DB 22; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||
QY 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFLLAQDI 120
   |||||||
Db 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFLLAQDI 120
   |||||||
QY 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||
Db 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||
QY 181 DNIRVNAISAGPIRTLSAKGVGFGNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSSG 240
   |||||||
Db 181 DNIRVNAISAGPIRTLSAKGVGFGNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSSG 240
   |||||||
QY 241 VTGENIHVDSGFHAIK 256
   |||||||
Db 241 VTGENIHVDSGFHAIK 256
   |||||||

RESULT 14
US-10-009-219-2
; Sequence 2, Application US/10009219
; GENERAL INFORMATION:
; APPLICANT: DEWOLF, WALTER E.
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS
; FILE REFERENCE: GMS0056
; CURRENT APPLICATION NUMBER: US/10/009,219
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PCT/US00/12104
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/134,362
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-009-219-2

Query Match      100.0%; Score 1277; DB 24; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||
Db 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||
QY 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFLLAQDI 120
   |||||||
Db 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFLLAQDI 120
   |||||||
QY 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||
Db 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||
QY 181 DNIRVNAISAGPIRTLSAKGVGFGNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSSG 240
   |||||||
Db 181 DNIRVNAISAGPIRTLSAKGVGFGNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSSG 240
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QY 241 VTGENIHVDSGFHAIK 256
   |||||||
Db 241 VTGENIHVDSGFHAIK 256
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RESULT 15
US-10-072-851-5228
; Sequence 5228, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit Proliferation
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,851
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5228
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-072-851-5228

Query Match      100.0%; Score 1277; DB 24; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
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Db 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||
QY 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFLLAQDI 120
   |||||||
Db 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFLLAQDI 120
   |||||||
QY 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||
Db 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||
QY 181 DNIRVNAISAGPIRTLSAKGVGFGNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSSG 240
   |||||||
Db 181 DNIRVNAISAGPIRTLSAKGVGFGNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSSG 240
   |||||||
QY 241 VTGENIHVDSGFHAIK 256
   |||||||
Db 241 VTGENIHVDSGFHAIK 256
   |||||||
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Search completed: September 22, 2002, 17:03:32
Job time: 3453 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2002, 16:07:04 ; Search time 100.11 Seconds
(without alignments)
684.068 Million cell updates/sec

Title: US-09-292-411A-2
Perfect score: 1277
Sequence: 1 MLNLENTYVIMGIANKRSI.....LSSGVGTGENIHVDSGFHAIK 256

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 947138 seqs, 267508082 residues

Total number of hits satisfying chosen parameters: 947138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	256	5	US-09-791-537-111094
2	1263	98.9	255	6	US-10-089-019-12
3	1186	90.5	256	6	US-10-138-701-6
4	796	62.3	259	7	US-60-360-039-16488
5	767	60.1	260	7	US-60-360-039-17364
6	749	58.7	258	5	US-09-791-537-130900
7	749	58.7	269	5	US-09-791-537-2330
8	749	58.7	269	7	US-60-360-039-17696
9	626.5	49.1	260	7	US-60-360-039-20054
10	624.5	48.9	258	5	US-09-791-537-62042
11	624.5	48.9	264	5	US-09-791-537-91445
12	624.5	48.9	264	7	US-60-360-039-18839
13	610	47.8	256	7	US-60-360-039-21754
14	591	46.3	254	7	US-60-360-039-17909
15	591	46.3	261	7	US-60-360-039-11750
16	591	46.3	261	7	US-60-360-039-14291
17	591	46.3	261	7	US-60-360-039-14486
18	591	46.3	261	7	US-60-360-039-14870
19	589	46.1	272	7	US-60-360-039-12287
20	586	45.9	254	7	US-60-360-039-20612
21	581	45.5	264	7	US-60-360-039-7881
22	578	45.3	261	7	US-60-360-039-10861
23	575	45.0	250	7	US-60-360-039-18344
24	572.5	44.8	258	5	US-09-791-537-44256
25	572.5	44.8	278	5	US-09-791-537-29789
26	572.5	44.8	278	7	US-60-360-039-2640

ALIGNMENTS

RESULT 1
US-09-791-537-111094
; Sequence 111094, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 111094
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-791-537-111094

Query Match 100.0%; Score 1277; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.5e-105;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLNLENTYVIMGIANKRSIAGFVAKVLDLGAKLVFTYRKRSRKELEKLEQLNQPEA 60
Db 1 MLNLENTYVIMGIANKRSIAGFVAKVLDLGAKLVFTYRKRSRKELEKLEQLNQPEA 60
QY 61 HLVDVDSDEEYNGFEQIGKDVGNIDGVYHSAFANNEDLGRFSETSGEFLAQDI 120
Db 61 HLVDVDSDEEYNGFEQIGKDVGNIDGVYHSAFANNEDLGRFSETSGEFLAQDI 120
QY 121 SSSSLTVAHEAKKLMEGGSIATVYTLGGFEFVQNTVMGVAKASLEANKYKYLALDLP 180
Db 121 SSSSLTVAHEAKKLMEGGSIATVYTLGGFEFVQNTVMGVAKASLEANKYKYLALDLP 180
QY 181 DNIIRVNAISAGPRTLSAKGVGGNTTLKETEERAPLKRNVQVQVEGKTAAYLLSDLSG 240
Db 181 DNIIRVNAISAGPRTLSAKGVGGNTTLKETEERAPLKRNVQVQVEGKTAAYLLSDLSG 240
QY 241 VTGENIHVDSGFHAIK 256
Db 241 VTGENIHVDSGFHAIK 256

RESULT 2
US-10-089-019-12
; Sequence 12, Application US/10089019

; GENERAL INFORMATION:

; APPLICANT: DEWOLF, WALTER E. JR
; APPLICANT: KALLENDER, HOWARD
; APPLICANT: LONSDALE, JOHN T.
; TITLE OF INVENTION: METHODS FOR MAKING AND USING FAULTY ACID
; TITLE OF INVENTION: SYNTHESIS PATHWAY REAGENTS

; FILE REFERENCE: GM50068

; CURRENT APPLICATION NUMBER: US/10/089,019

; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER: PCT/US00/29451

; PRIOR FILING DATE: 2000-10-26

; PRIOR APPLICATION NUMBER: 60/161,775

; PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 255

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-10-089-019-12

Query Match 98.9%; Score 1263; DB 6; Length 255;

Best Local Similarity 100.0%; Pred. No. 4.3e-104;

Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEAH 61

Db 3 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEAH 62

Qy 62 LYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFFLLAQDIS 121

Db 63 LYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFFLLAQDIS 122

Qy 122 SYSLSIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAKASLEANVYALDLDGPD 181

Db 123 SYSLSIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAKASLEANVYALDLDGPD 182

Qy 182 NIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQVEVGKTAAYLLSDLSGV 241

Db 183 NIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQVEVGKTAAYLLSDLSGV 242

Qy 242 TGENIHVDSGFHA 254

Db 243 TGENIHVDSGFHA 255

RESULT 3

US-10-138-701-6

; Sequence 6, Application US/10138701

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides

; FILE REFERENCE: P8484

; CURRENT APPLICATION NUMBER: US/10/138,701

; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: US/09/512,255A

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/098,964

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: US 60/009,861

; PRIOR FILING DATE: 1996-01-05

; PRIOR APPLICATION NUMBER: PCT/ US99/19726

; PRIOR FILING DATE: 1999-08-31

; PRIOR APPLICATION NUMBER: US 08/956,171

; PRIOR FILING DATE: 1997-10-20

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 256

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-10-138-701-6

Query Match

Best Local Similarity 90.5%; Score 1156; DB 6; Length 256;

Matches 239; Conservative 0; Mismatches 1; Indels 32; Gaps 2;

Qy 1 MLNENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEA 60

Db 1 MLNENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEA 60

Qy 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAF-----ANMEDLGR 104

Db 61 HLYQ-----GKDVGNIDGVYHSIAFIDVQSDVEEVINGFEQIANMEDLGR 104

Qy 105 RSETSRGFFLLAQDISYSLSIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAK 164

Db 105 RSETSRGFFLLAQDISYSLSIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAK 164

Qy 165 ASLEANVYALDLDGPDNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQV 224

Db 165 ASLEANVYALDLDGPDNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQV 224

Qy 225 EVGKTAAYLLSDLSGVTGENIHVDSGFHA 256

Db 225 EVGKTAAYLLSDLSGVTGENIHVDSGFHA 256

RESULT 4

US-60-360-039-16488

; Sequence 16488, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 16488

; LENGTH: 259

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-60-360-039-16488

Query Match

Best Local Similarity 62.3%; Score 796; DB 7; Length 259;

Matches 159; Conservative 38; Mismatches 53; Indels 0; Gaps 0;

Qy 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEAH 63

Db 9 LQKTFVYVGVANOKSIAGIARSLHNAKLIIFTYAGERLERNVRELADTLEGOESLV 68

Qy 64 QIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFFLLAQDIS 123

Db 69 PCDVTNDEELTACFETIKQEVGTIHGVAHCIAFANRDLKGEFVDTSRDGLLAQNISAF 128

Qy 124 SLTIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAKASLEANVYALDLDGPDNI 183

Db 129 SLTAVAREAKKVMTEGGNLTLYLGGERVVKNYVNMVAKASLEASVKYLANDLGQHG 188

Qy 184 RVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQVEVGKTAAYLLSDLSGVTG 243

Db 189 RVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQVEVGKTAAYLLSDLSGVTG 248

Qy 244 ENIHVDSGFH 253

Db 249 ENIHVDSGFH 258

RESULT 5
US-60-360-039-17364
; Sequence 17364, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17364
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-60-360-039-17364

Query Match 60.1%; Score 767; DB 7; Length 260;
Best Local Similarity 60.6%; Pred. No. 5, 2e-60;
Matches 154; Conservative 41; Mismatches 59; Indels 0; Gaps 0;
QY 2 NLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLEQLNQPEAHL 61
DB 4 LSLVDRTYVVMGVANKRSIAWGIAQSLANAGARLIIFTYAGERLEKNVGRVLVETLRDDHL 63
QY 62 LQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGREGFLAODISS 121
DB 64 VLECDVTSDEAVTEATPASKIEQVGTIHGLAHCIATAFANKEELGEGEYLNTTRDGFLLAHNIS 123
QY 122 YSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVONVYVGVAKASLEAVNKYLLALDLPD 181
DB 124 AVSLTAVAKAARPLMNEGGSIVTLTYLGGEKVYVNVYVGVAKASLDASVKYLLANDLGKE 183
QY 182 NRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLNVDQVEVGKTAAYLLSDLSGGV 241
DB 184 NRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLNVDQVEVGKTAAYLLSDLSGGV 243
QY 242 TGENIHDVDSGFH 255
DB 244 TGEILHVDVSGFNL 257

RESULT 6
US-09-791-537-130900
; Sequence 130900, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 130900
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-791-537-130900
Query Match 58.7%; Score 749; DB 5; Length 258;
Best Local Similarity 59.0%; Pred. No. 2e-58;
Matches 148; Conservative 41; Mismatches 62; Indels 0; Gaps 0;

QY 3 NLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLEQLNQPEAHL 62
DB 4 LSEGRNVVMGVANKRSIAWGIAQSLANAGARLIIFTYAGERLEKNVGRVLVETLRDDHL 63
QY 63 YQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGREGFLAODISS 122
DB 64 LPCDVTNDAAEIEITCFASIKQVGVHIGIAHCIAFANKEELVGEYLNTRDGFLLAHNIS 123
QY 123 YSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVONVYVGVAKASLEAVNKYLLALDLPD 182
DB 124 YSLTAVVAKAARPMTEGGGSIVTLTYLGGEVMPNYPNVYVGVAKASLDASVKYLLADLGKE 183
QY 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLNVDQVEVGKTAAYLLSDLSGGV 242
DB 184 IRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLNVDQVEVGKTAAYLLSDLSGGV 243
QY 243 GENIHDVDSGFH 253
DB 244 GENLHVDVSGFH 254
RESULT 7
US-09-791-537-2330
; Sequence 2330, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2330
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-791-537-2330

Query Match 58.7%; Score 749; DB 5; Length 269;
Best Local Similarity 59.0%; Pred. No. 2, 2e-58;
Matches 148; Conservative 41; Mismatches 62; Indels 0; Gaps 0;
QY 3 NLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLEQLNQPEAHL 62
DB 15 SLEGRNVVMGVANKRSIAWGIAQSLANAGARLIIFTYAGERLEKNVGRVLVETLRDDHL 74
QY 63 YQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGREGFLAODISS 122
DB 75 LPCDVTNDAAEIEITCFASIKQVGVHIGIAHCIAFANKEELVGEYLNTRDGFLLAHNIS 134
QY 123 YSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVONVYVGVAKASLEAVNKYLLALDLPD 182
DB 135 YSLTAVVAKAARPMTEGGGSIVTLTYLGGEVMPNYPNVYVGVAKASLDASVKYLLADLGKE 194
QY 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLNVDQVEVGKTAAYLLSDLSGGV 242
DB 195 IRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLNVDQVEVGKTAAYLLSDLSGGV 243
QY 243 GENIHDVDSGFH 253
DB 255 GENLHVDVSGFH 265

RESULT 8
US-60-360-039-17696
; Sequence 17696, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17696
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-60-360-039-17696

Query Match 58.7%; Score 749; DB 7; Length 269;
Best Local Similarity 59.0%; Pred. No. 2.2e-58;
Matches 148; Conservative 41; Mismatches 62; Indels 0; Gaps 0;

Qy 3 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTYRKSRKELEKLEQLNOPEAHL 62
Db 15 SLEGNIVVMGVANKRSTANGIARSLHAGARLIYTAGERLEKSVHELACTLDRNDSII 74
Qy 63 YQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSREGFLA 122
Db 75 LPCDVTDAEITCFASIKQGVGTHGIAHCFATFANKEELVGYLNTNRDGFLLAHNISS 134
Qy 123 YSLTVAHEAKLMPEGGSIATVTLGGGFVQNVNMGVAKASLEANKYLALDLPDN 182
Db 135 YSLTAVKAAAPMTGGSIATVTLGGELVMPNVMGVAKASLDASVKYLAADLGKEN 194
Qy 183 IRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSGVT 242
Db 195 IRVNSISAGPIRTLSAKGISDFNSILKDIERAPLRRTTPEEVGDTAAFLFSDMSRGIT 254
Qy 243 GENTHVDSGFH 253
Db 255 GENTHVDSGFH 265

RESULT 9
US-60-360-039-20054
; Sequence 20054, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 20054
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Nostoc punctiforme
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(260)
; OTHER INFORMATION: unsure at all xaa locations
US-60-360-039-20054

Query Match 49.1%; Score 626.5; DB 7; Length 260;
Best Local Similarity 52.5%; Pred. No. 1.6e-47;
Matches 134; Conservative 45; Mismatches 71; Indels 5; Gaps 3;

Qy 1 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTY---RKERSRKELEKLEQLNQ 57
Db 11

Db 3 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTY---RKERSRKELEKLEQLNQ 61
Qy 58 PEALHYQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSREGFLA 117
Db 62 PSFL-PCNVQDSEIQITFTIIRQWGLDILHCLAFASKDDLSGDFQSRSRGFSTA 120
Qy 118 QDISSYSLTVAHEAKLMPEGGSIATVTLGGGFVQNVNMGVAKASLEANKYLALD 177
Db 121 LEISTYSLVOLSGAAKPLMTGGSIATVTLGGVRAIPNVMGVAKAGLEMSVRYLAEE 180
Qy 178 LGPNIRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSD 237
Db 181 LGPNIRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSD 240
Qy 238 SSGVTGENIHVDSGF 252
Db 241 SSGITGQVLYVDAGY 255

RESULT 10
US-09-791-537-62042
; Sequence 62042, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Danzer, Joseph
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62042
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Anabaena PCC7120
US-09-791-537-62042

Query Match 48.9%; Score 624.5; DB 5; Length 258;
Best Local Similarity 52.2%; Pred. No. 2.3e-47;
Matches 133; Conservative 47; Mismatches 70; Indels 5; Gaps 3;

Qy 1 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTY---RKERSRKELEKLEQLNQ 57
Db 1 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTY---RKERSRKELEKLEQLNQ 59
Qy 58 PEALHYQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSREGFLA 117
Db 60 PSFL-PCNVQDSEIQITFTIIRQWGLDILHCLAFASKDDLSGDFQSRSRGFSTA 118
Qy 118 QDISSYSLTVAHEAKLMPEGGSIATVTLGGGFVQNVNMGVAKASLEANKYLALD 177
Db 119 LDISTFSLVOLSGAAKPLMTGGSIATVTLGGVRAIPNVMGVAKAGLEMSVRYLAEE 178
Qy 178 LGPNIRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSD 237
Db 179 LGPNIRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSD 238
Qy 238 SSGVTGENIHVDSGF 252
Db 239 ASGITGQVLYVDAGY 253

RESULT 11
US-09-791-537-91445
; Sequence 91445, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

;; TITLE OF INVENTION: METHODS OF USE THEREOF
;; FILE REFERENCE: 261/210
;; CURRENT APPLICATION NUMBER: US/09/791,537
;; CURRENT FILING DATE: 2001-02-22
;; NUMBER OF SEQ ID NOS: 153055
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 91445
;; LENGTH: 264
;; TYPE: PRT
;; ORGANISM: Nostoc sp
US-09-791-537-91445

Query Match 48.9%; Score 624.5; DB 5; Length 264;
Best Local Similarity 52.2%; Pred. No. 2.4e-47;
Matches 133; Conservative 47; Mismatches 70; Indels 5; Gaps 3;

QY 1 MLNLENTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTY---RKERSRKELEKLEQLNQ 57
DB 7 MLNLTGKNAVLTGIANNRSIAWIAQOLHAAGANLIGITYLPDRGKFEKVSSELVEPLN- 65
QY 58 PEARLQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSHAFANMEDLRGRFSETSGREGFLA 117
DB 66 PSFLF-PCNVQNDQIQSTEDTIRDKWGRDLILHCLAFANRDLDTGDFQTSRAGFATA 124
QY 118 QDISSTSLTTVAHEAKLMPEGGSIATVTLGGEFAVQNTVNMGVAKASLEANKYALD 177
DB 125 LDISTFSLVOLSGAAKPLMTEGGSIITLSYLGVRVAVPNTVNMGVAKASLEANSVRYLASE 184
QY 178 LGPDNIRVNIAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDL 237
DB 185 LGSQNIIRVNIAISAGPIRTLSASSAVGGILDMIHVHVEQVA2LRRTVTQLEVGNVTAFLASDL 244

QY 238 SSGVTGENIHVDSGF 252
DB 245 ASGITGVLYVDAGY 259

RESULT 12
US-60-360-039-18839
; Sequence 18839, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18839
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Anabaena PCC7120
US-60-360-039-18839

Query Match 48.9%; Score 624.5; DB 7; Length 264;
Best Local Similarity 52.2%; Pred. No. 2.4e-47;
Matches 133; Conservative 47; Mismatches 70; Indels 5; Gaps 3;

QY 1 MLNLENTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTY---RKERSRKELEKLEQLNQ 57
DB 7 MLNLTGKNAVLTGIANNRSIAWIAQOLHAAGANLIGITYLPDRGKFEKVSSELVEPLN- 65
QY 58 PEARLQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSHAFANMEDLRGRFSETSGREGFLA 117
DB 66 PSFLF-PCNVQNDQIQSTEDTIRDKWGRDLILHCLAFANRDLDTGDFQTSRAGFATA 124
QY 118 QDISSTSLTTVAHEAKLMPEGGSIATVTLGGEFAVQNTVNMGVAKASLEANKYALD 177

DB 125 LDISTFSLVOLSGAAKPLMTEGGSIITLSYLGVRVAVPNTVNMGVAKASLEANSVRYLASE 184
QY 178 LGPDNIRVNIAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDL 237
DB 185 LGSQNIIRVNIAISAGPIRTLSASSAVGGILDMIHVHVEQVA2LRRTVTQLEVGNVTAFLASDL 244

QY 238 SSGVTGENIHVDSGF 252
DB 245 ASGITGVLYVDAGY 259

RESULT 13
US-60-360-039-21754
; Sequence 21754, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21754
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Rhodobacter capsulatus
US-60-360-039-21754

Query Match 47.8%; Score 610; DB 7; Length 256;
Best Local Similarity 49.6%; Pred. No. 4.5e-46;
Matches 125; Conservative 44; Mismatches 81; Indels 2; Gaps 1;

QY 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLEQLNOPEAHLY 63
DB 6 MAGKRGILMGLANDKSIWAGIAKALGADAGAEAFSYQGHALKKRVEPLAASLGTP--LLF 63
QY 64 QIDVQSDVEEVINGFEQIGKDVGNIDGVYHSHAFANMEDLRGRFSETSGREGFLAQQDISY 123
DB 64 ECDVANEDSDALFAGLKDAMGTLDLVYHAIQFSDKNELRGYVDTSRGNFTMTDISVY 123
QY 124 SLTIVAHEAKLMPEGGSIATVTLGGEFAVQNTVNMGVAKASLEANKYALDLGPDNI 183
DB 124 SFTAVCARAAAMPNGGSLTLTYGAEQVMPHYNMGVAKAALASVKYIAEDLGKGI 183
QY 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSSGVG 243
DB 184 RCNAISAGPIKTLAASGIGDFRYIMKNELNPLRRNVQEEVGKAAALLSLLSGSGTG 243

QY 244 ENIHVDSGFPHAI 255
DB 244 ENLHVDAHYHV 255

RESULT 14
US-60-360-039-17909
; Sequence 17909, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21

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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 15:11:13 ; Search time 47.08 Seconds
(without alignments)
4022.588 Million cell updates/sec

Title: US-09-292-411a-1
Perfect score: 771
Sequence: 1 atgttaaatcttgaacaa.....gattccacgcaataataa 771

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54.2	7.0	1173	US-09-586-719-1	Sequence 1, Appli
2	50.2	6.5	741	US-09-238-481-1	Sequence 1, Appli
3	41.4	5.4	4198	US-09-586-719-11	Sequence 11, Appli
4	39.4	5.1	3763	US-07-792-865D-1	Sequence 1, Appli
5	39.2	5.1	797	US-08-752-132-1	Sequence 1, Appli
6	39	5.1	1891	US-08-973-462-3	Sequence 3, Appli
7	39	5.1	5361	US-08-973-462-2	Sequence 2, Appli
8	39	5.1	6152	US-08-973-462-1	Sequence 1, Appli
9	38.8	5.0	951	US-09-241-750-1	Sequence 1, Appli
10	38	4.9	5910	US-08-195-814-1	Sequence 1, Appli
11	38	4.9	7218	US-08-232-463-14	Sequence 14, Appli
12	37.6	4.9	1251	US-09-007-476-1	Sequence 1, Appli
13	37.6	4.9	2483	US-08-526-964-1	Sequence 1, Appli
14	37.6	4.9	2483	US-08-946-617-1	Sequence 5, Appli
15	37.6	4.9	2483	US-09-031-897-1	Sequence 1, Appli
16	37.6	4.9	5203	US-09-257-770-1	Sequence 1, Appli
17	37.2	4.8	7493	US-08-212-133A-7	Sequence 7, Appli
18	37.2	4.8	7493	US-08-474-503-5	Sequence 5, Appli
19	37.2	4.8	7493	US-08-670-707A-5	Sequence 5, Appli
20	37.2	4.8	7493	US-09-037-601-5	Sequence 5, Appli
21	37.2	4.8	7493	PCT-US94-13200-5	Sequence 5, Appli
22	36.8	4.8	824	US-08-158-353-1	Sequence 1, Appli
23	36	4.7	2301	US-09-561-825-1	Sequence 1, Appli
24	36	4.7	2361	US-09-561-825-26	Sequence 26, Appli
25	36	4.7	2361	US-09-561-825-29	Sequence 29, Appli
26	36	4.7	2362	US-09-561-825-27	Sequence 27, Appli
27	36	4.7	2363	US-09-561-825-28	Sequence 28, Appli

28	35.8	4.6	2101	2	US-08-568-459A-9	Sequence 9, Appli
29	35.8	4.6	2101	2	US-08-487-826B-9	Sequence 9, Appli
30	35.8	4.6	7295	2	US-08-487-826B-15	Sequence 15, Appli
31	35.6	4.6	654	4	US-08-936-165A-234	Sequence 234, App
32	35.6	4.6	1431	4	US-09-316-083-2	Sequence 2, Appli
33	35.4	4.6	7101	1	US-08-480-604A-9	Sequence 9, Appli
34	35.4	4.6	7101	2	US-08-405-496A-9	Sequence 9, Appli
35	35.4	4.6	7101	4	US-08-915-136-9	Sequence 9, Appli
36	35.2	4.6	1830	3	US-08-933-750C-79	Sequence 79, Appli
37	35.2	4.6	1830	3	US-09-234-613-79	Sequence 79, Appli
38	35	4.5	1601	3	US-09-038-909-1	Sequence 1, Appli
39	35	4.5	3879	1	US-08-530-010-1	Sequence 1, Appli
40	35	4.5	3879	1	US-08-484-101B-1	Sequence 1, Appli
41	35	4.5	3879	4	US-08-714-524D-1	Sequence 1, Appli
42	35	4.5	5319	1	US-08-169-927-1	Sequence 1, Appli
43	34.8	4.5	1500	4	US-08-856-253-5	Sequence 5, Appli
44	34.8	4.5	3827	2	US-08-447-031A-1	Sequence 1, Appli
45	34.8	4.5	4612	2	US-08-447-031A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-586-719-1
; Sequence 1, Application US/09586719
; Patent No. 6294345
; GENERAL INFORMATION:
; APPLICANT: Zheng, Feng
; APPLICANT: Levin, Joshua Z.
; APPLICANT: Bauer, Michael W.
; TITLE OF INVENTION: Herbicide Target Genes and Methods
; FILE REFERENCE: PB/5-30909A
; CURRENT APPLICATION NUMBER: US/09/586,719
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1173)
US-09-586-719-1

Query Match	7.0%	Score 54.2;	DB 4;	Length 1173;
Best Local Similarity	52.5%	Pred. No. 8.5e-06;		
Matches 116;	Conservative 1;	Mismatches 104;	Indels 0;	Gaps 0;
QY	544	aatattcggttaattcaatttcagctgtgtcccaatcgctacattagtgcaaaagtggtg	603	
Db	901	aacattagggtcaacaccatatctgcgggtctcttgggaagcgcagcagcaaaagccatt	960	
QY	604	ggtggtttcaatacaattctttaaagaatacgaagagcgtgcacctttaaacgtaacgtt	663	
Db	961	gggttcatacacaccatgattgagttatctcacaataatgacctattcagaaacactg	1020	
QY	664	gatcaagtgaagttagtataaacacagcggcttactttttaagtgaacttatcaagtgcgtt	723	
Db	1021	accgcagagaaggttggaatgcagcagcctctcttgccattggcctctgcata	1080	
QY	724	acaggtgaaaattattcatgtagtagcggattccacgcaat	764	
Db	1081	accggtgcaaccatatatgtggacaatggttgaatgcaat	1121	

RESULT 2
US-09-238-481-1
; Sequence 1, Application US/09238481
; Patent No. 6110704
; GENERAL INFORMATION:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-526-964-1

Query Match 4.9%; Score 37.6; DB:1; Length 2483;
Best Local Similarity 47.1%; Pred. No. 0.35;
Matches 115; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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DB 1156 CTGGATATGTTGATAAAATAATAATATCATAATACACTTTAGGAATTCCTCAAGGTA 1215

QY 122 aagaacgtagcgcgaagcgcttgaaaaattatttagaacaattaaatcaaccagaagcgc 181
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QY 182 acttatcaaatgttgctcaagcgatgaagaggttatttaattggttttgacaaattg 241
DB 1276 ATAAATTTGAGAAATGAATCAACTACTGGAATATGCTTAATAGAGGTAGAAATCCAAATTT 1335

QY 242 gtaa 245
DB 1336 ATAA 1339

RESULT 14
US-08-946-617-1
Sequence 5, Application US/08911320A
Patent No. 5869633
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
TITLE OF INVENTION: THROMBIN RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,320A
FILING DATE: August 14, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,125
FILING DATE: 6-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0041-1 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-4170
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
Sequence 1, Application US/08946617
Patent No. 5869634
GENERAL INFORMATION:
APPLICANT: Lambowitz, Alan M
APPLICANT: Zimmerly, Steven
APPLICANT: Guo, Huatao
APPLICANT: Yang, Jian
TITLE OF INVENTION: Nucleotide Integrase Preparation
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: USA
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,617
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gorrlick, Mary E
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-946-617-1

Query Match 4.9%; Score 37.6; DE 2; Length 2483;
Best Local Similarity 47.1%; Pred. No. 0.35;
Matches 115; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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; Sequence 1, Application US/09031897
; Patent No. 6027895
; GENERAL INFORMATION:
; APPLICANT: Lambowitz, Alan
; APPLICANT: Mohr, Georg
; APPLICANT: Zimmerly, Steven
; APPLICANT: Guo, Huatao
; TITLE OF INVENTION: Methods Cleaving DNA with Nucleotide
; TITLE OF INVENTION: Integrases
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griswold
; STREET: 800 Superior Avenue, Suite 1400
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031.897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40,591
; REFERENCE/DOCKET NUMBER: 24671/00105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216)622-8416
; TELEFAX: (216)241 0816
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
US-09-031-897-1

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Db 1096 TATTAATGAGAGAAATCAAGATTAAGGTTTCATAGACTTATTATATAAATTATTAGAG 1155
Qy 62 cttttggtgcgtaaggttttagatcaattagggtgtaaataggtagttactaccgta 121
Db 1156 CTGGATATGTTGATAAAATAAATAATTATCATATAACAACCTTAGGAATTCCTCAAGGTA 1215
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Qy 182 acttatcaaatgtgttcaagcgatgaagaggttatttaattggtttgagcaaatg 241
Db 1276 ATAAATTTGAGATGAATCAATCAATCTGGAATATGCTAATAGAGGTAGAAATCAATTT 1335
Qy 242 gtaa 245
Db 1336 ATAA 1339

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 15:12:28 ; Search time 2795.16 Seconds
(without alignments)
5967.639 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	770.6	99.9	771	11	US-08-790-043A-2
3	770.6	99.9	771	11	US-08-790-043B-1
4	770.6	99.9	771	16	US-09-292-411A-1
5	770.6	99.9	771	16	US-09-292-411A-1
6	770.6	99.9	771	16	US-09-292-412-1
7	767.6	99.6	774	1	PCT-US00-29451-11
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9	762.6	98.9	771	31	US-09-815-242-8794
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11	761	98.7	916	1	PCT-US99-19726-5
12	761	98.7	916	19	US-09-512-255-5
13	761	98.7	916	19	US-09-512-255A-5
14	756.6	98.1	775	1	PCT-US00-12104-1
15	756.6	98.1	775	37	US-10-009-219-1
16	755.6	98.0	1167	1	PCT-US97-02318-1110
17	755.6	98.0	1167	13	US-08-903-470-1110
18	749.8	97.3	771	1	PCT-US02-03987-8437
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20	749.8	97.3	771	37	US-10-072-851-8437
21	746.8	96.9	768	1	PCT-US02-03987-4173
22	746.8	96.9	768	31	US-09-815-242-4173
23	746.8	96.9	768	37	US-10-072-851-4173
24	743	96.4	792	16	US-09-266-555-7
25	743	96.4	795	23	US-09-611-529-58
26	743	96.4	278942	23	US-09-611-529-7437
27	734.6	95.3	77711	12	US-08-831-156A-105
28	645	83.7	704	11	US-08-781-986A-772
29	645	83.7	704	13	US-08-956-171-772
30	645	83.7	704	13	US-08-956-171B-772
31	645	83.7	704	13	US-08-956-171C-772


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; APPLICATION NUMBER: US/08/790,043A
; FILING DATE: 28-August-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024845
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Glimi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: GM50005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-790-043A-2

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Qy	61	gctttgggtgcgtctaaagttttagatcaaatagggtgctaaattagttatttactaccgt	120				
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Qy	181	cacttatatacaaatgtgatttcaaaagcgtgaaagaggttataatggttttgagcaaat	240				
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RESULT 3
; Sequence 1, Application US/08790043B
; GENERAL INFORMATION:
; APPLICANT: Payne, David
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: FAB I
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,043B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,845
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM50005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-790-043B-1

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	Query Match	99.9%;	Score	770.6;	DB	11;	Length	771;
	Best Local Similarity	100.0%;	Prod.	No. 1.8e-177;				
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US-09-292-411-1
; Sequence 1, Application US/09292411
; GENERAL INFORMATION:
; APPLICANT: Payne, David
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: FAB I
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch St
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/292,411
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/790,043
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM50005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488

; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-292-411-1

Query Match 99.9%; Score 770.6; DB 16; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.8e-177;
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaaatcttgaaacaaacacatatgtcatcattggtggaatcgctaaataagcgtagtatt 60
Db 1 ATGTTAAATCTTGAACAAACAAACATATGTCAATCGGAATCGCTAATAAGCGTAGTATT 60
QY 61 gcttttggtgcgtctaaagtttttagatcaattagtgctcaaatagttatttacttaccgt 120
Db 61 GCTTTTGGTGTGCGCTTAAAGTTTGTAGTCAATTAGTGTCTAAATTTAGTATTACTTACCCT 120
QY 121 aaagaacgtagcgttaagagcgttgaaataattattagaacaaattaaatcaaccagaagcg 180
Db 121 AAAGAACGTAGCGCTTAAAGAGCTTGAAAAATTTATTAGAACAATTTAAATCAACCAAGCG 180
QY 181 cacttatatacaattgatgttcaaaagcgtgaagaggttatttaaggttttgagcaaat 240
Db 181 CACTTATATCAAAATTTGATGTTCAAGCGATGAAGAGGTTATTAAATGGTGTGAGCAAAAT 240
QY 241 ggttaagatgttgcaaatattgatgtgtatatcatcattcaatcgcatcttgctaatatgaa 300
Db 241 GGTAAAGATGTTGGCAATATTGATGCTGTATATCATTTCAATCGCAATTTGCTAATAATGGA 300
QY 301 gacttacgagcgttcttgaaacttcacgtgaagcgttctttagctcaagacatt 360
Db 301 GACTTACGCGGACGCTTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGTCAAGACATT 360
QY 361 agtcttactcaatacaattgtggtcgtcatgaagctaaataataatgccagaagtggt 420
Db 361 AGTCTTACTCAATTAACCAATTTGGCTCATGAAGCTAATAATAATTAATGCCAGAAGTGCT 420
QY 421 agcattgttgcaacacacatatatttagtggtgcgaattcgcagttcgaataataataatgatg 480
Db 421 AGCAATGTTGCAACAACATATTATTAGTGGCGAATTCGCAGTTCAAAATTAATAATGATG 480
QY 481 ggtgttgctaaagcgtttagaagcaaatgttaaatatttagcatttaggttccct 540
Db 481 GGTGTGCTAAAGCGAGCTTGAAGCAAAATGTTAAATATTAGCAATTTAGCACTTAGGTCT 540
QY 541 gataatattcggttaattcaatttcagctggtccaatccgtacattagtgcaaaaggt 600
Db 541 GATAATATTCGCGTTAATGCAATTTACGTGCTCAATCCGTACATTAAGTGCAAAAGGT 600
QY 601 gttggtgtttcaatacaattctttaaagaattcgaagcgtgcaccttttaaacgttaac 660
Db 601 GTGGGTGTTTCAATACAAATCTTAAGCAAAATCGAAGAGCGTGCCACCTTTAAACGTTAAC 660
QY 661 gttgataagtagaagtaggttaaaacagcgttacttrttaagtgacttatcaagtgcc 720
Db 661 GTTGATCAAGTAGAAGTAGTAAACACAGCGGCTTACTTTRTAAGTGACTTATCAAGTGGC 720
QY 721 gttacagtgaaataattcatgtagatgacgagattccacgaattaaataa 771
Db 721 GTTACAGTGAAATATTCAATGATAGCGGATTTCCACGCAATTAATAA 771

RESULT 5

US-09-292-411A-1
; Sequence 1, Application US/09292411A
; GENERAL INFORMATION:
; APPLICANT: Lonsdale, John

APPLICANT: Milner, Peter
APPLICANT: Payne, David
APPLICANT: Pearson, Stewart
TITLE OF INVENTION: Fabi
FILE REFERENCE: GM50005-D1
CURRENT APPLICATION NUMBER: US/09/292,411A
CURRENT FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 08/790,043
PRIOR FILING DATE: 1997-01-28
PRIOR APPLICATION NUMBER: US 60/024,845
PRIOR FILING DATE: 1996-08-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 771
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-292-411A-1

Query Match 99.9%; Score 770.6; DB 16; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.8e-177;
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaaatcttgaaacaaacataatgcatcattggaatcgctaaatagcgtatgatt 60
DB 1 atgttaaatcttgaaacaaacataatgcatcattggaatcgctaaatagcgtatgatt 60
QY 61 gcttttggtgctgctaaagtctttagatcaatgagtgctaaatagctattaccgt 120
DB 61 gcttttggtgctgctaaagtctttagatcaatgagtgctaaatagctattaccgt 120
QY 121 aaagaacgtagcgtgaaagcgttgaaatattattagaacaattaaatcaacagaagcg 180
DB 121 aaagaacgtagcgtgaaagcgttgaaatattattagaacaattaaatcaacagaagcg 180
QY 181 caattatacaaatgattgctaaacgcatgaagaggttatttaattggttgagcaaat 240
DB 181 caattatacaaatgattgctaaacgcatgaagaggttatttaattggttgagcaaat 240
QY 241 ggtcaagatggtgcaatattggtgctatcatcattcgaatcgcttgcataatggaa 300
DB 241 ggtcaagatggtgcaatattggtgctatcatcattcgaatcgcttgcataatggaa 300
QY 301 gacttacgagcgtcttctgaaactcagctgaaaggtcttctgtagctcaagacatt 360
DB 301 gacttacgagcgtcttctgaaactcagctgaaaggtcttctgtagctcaagacatt 360
QY 361 agttcttactcattaaacattggtgctcatgaagcgttaaaatattgccaagagtggt 420
DB 361 agttcttactcattaaacattggtgctcatgaagcgttaaaatattgccaagagtggt 420
QY 421 agcattgtgcaacaacataattgagtggtgctgcaatcgagttcaaaattataatgtag 480
DB 421 agcattgtgcaacaacataattgagtggtgctgcaatcgagttcaaaattataatgtag 480
QY 481 ggtgtgtgctaaagcgttagaagcaaatgttaaatatttagcatttagacttagtcct 540
DB 481 ggtgtgtgctaaagcgttagaagcaaatgttaaatatttagcatttagacttagtcct 540
QY 541 gataatttcgcttaaatgcaatttcagctggtcccaatcgctacattagtgcaaaaggt 600
DB 541 gataatttcgcttaaatgcaatttcagctggtcccaatcgctacattagtgcaaaaggt 600
QY 601 gtgggtggtttcaatacaattcttaagaaatcgagagcgtgacgtcttaaaacgttaac 660
DB 601 gtgggtggtttcaatacaattcttaagaaatcgagagcgtgacgtcttaaaacgttaac 660
QY 661 gttgatcaagtagaagtaggttaaaacagcggcttactttrtttaagtgaacttatcaatggc 720
DB 661 gttgatcaagtagaagtaggttaaaacagcggcttactttrtttaagtgaacttatcaatggc 720
QY 721 gttacaggtgaaatattcattgtagatagcggattccacgcgaattaaataa 771

DB 721 gttacaggtgaaatattcattgtagatagcggattccacgcgaattaaataa 771
RESULT 6
US-09-292-412-1
Sequence 1, Application US/09292412
GENERAL INFORMATION:
APPLICANT: Payne, David
APPLICANT: Lonsdale, John
APPLICANT: Milner, Peter
APPLICANT: Pearson, Stewart
TITLE OF INVENTION: FAB I
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/292,412
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/790,043
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM50005
TELEPHONE: 215-994-2488
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-292-412-1
Query Match 99.9%; Score 770.6; DB 16; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.8e-177;
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaaatcttgaaacaaacataatgcatcattggaatcgctaaatagcgtatgatt 60
DB 1 atgttaaatcttgaaacaaacataatgcatcattggaatcgctaaatagcgtatgatt 60
QY 61 gcttttggtgctgctaaagtctttagatcaatgagtgctaaatagctattaccgt 120
DB 61 gcttttggtgctgctaaagtctttagatcaatgagtgctaaatagctattaccgt 120
QY 121 aaagaacgtagcgtgaaagcgttgaaatattattagaacaattaaatcaacagaagcg 180
DB 121 aaagaacgtagcgtgaaagcgttgaaatattattagaacaattaaatcaacagaagcg 180
QY 181 caattatacaaatgattgctaaacgcatgaagaggttatttaattggttgagcaaat 240
DB 181 caattatacaaatgattgctaaacgcatgaagaggttatttaattggttgagcaaat 240
QY 241 ggtcaagatggtgcaatattggtgctatcatcattcgaatcgcttgcataatggaa 300
DB 241 ggtcaagatggtgcaatattggtgctatcatcattcgaatcgcttgcataatggaa 300

QY 301 gacttaacgagcgctttctgaaacttcaagtggaaggtcttctttagctcaagacatt 360
|||||
Db 301 GACTTACGCGGACGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
|||||
QY 361 agttcttactcaataaattgtggtcgtcatgaagctaaataaattccaggaaggtggt 420
|||||
Db 361 AGTTCTTACTCATTAACAAATTGTGCTCATGAAGCTAAATAATTAATGCCAAGGTGGT 420
|||||
QY 421 agcattgtgcaacaacattattaggtggtggaattcgcagttcgaataataataatgtgatg 480
|||||
Db 421 AGCATTTGTCACAAACATATTTAGTGGCGAATTCGCGAGTTCAAAATTAATATGTGATG 480
|||||
QY 481 ggtgtgtgtaagcgagcttagaagcaaatgttaaatatttagcattagacttagtgcct 540
|||||
Db 481 GGTGTGTGCTAAGCGAGCTTAGAAGCAAAATGTTAAATATTATAGCATTAGACTTAGTCTCT 540
|||||
QY 541 gataaattcgcgttaataatgcaatttcagctggtcccaatccgtacatttaagtcgaaggt 600
|||||
Db 541 GATAAATATTCGCTTAAATGCAATTTACGCTGCTCCAAATCCGTACATTAAAGTCAAAAGGT 600
|||||
QY 601 gtgggtgtgtcaatacacaattcttaagaataatcgaagcgctgcaccttttaaacgtaac 660
|||||
Db 601 GTGGGTGTTCAATACAAATTTCTTAAGCAAAATCGAAGACGCTGCACCTTTAAACGTAAC 660
|||||
QY 661 gttgatcaagtagaagtaggttaaacacagcggtcttacttrttaagtgaacttatcaagtggc 720
|||||
Db 661 GTTGATCAAGTAGAAGTAGTAAAGTAAACAGCGGCTTACTTTRTTAAGTGACTTATCAAGTGGC 720
|||||
QY 721 gttacagtgaaataattcattcgtatgtagagcggtattccacgaataataaa 771
|||||
Db 721 GTTACAGTGAAATATTTTCATGTAGATAGCGGATTCACGCAATTAATAA 771
|||||

RESULT 7

PCT-US00-29451-11
; Sequence 11, Application PC/TUS0029451
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: METHODS FOR MAKING AND USING FATTY ACID
; TITLE OF INVENTION: SYNTHESIS PATHWAY REAGENTS
; FILE REFERENCE: CM50068
; CURRENT APPLICATION NUMBER: PCT/US00/29451
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/161,775
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
PCT-US00-29451-11

Query Match 99.6%; Score 767.6; DB 1; Length 774;
Best Local Similarity 100.0%; Pred. No. 9.6e-177;
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ttaaatcttgaaacaaacatatgtcatcgtgggaatcgctaatgaagcgtagtattgct 63
|||||
Db 7 ttaaatcttgaaacaaacatatgtcatcgtgggaatcgctaatgaagcgtagtattgct 66
|||||
QY 64 ttgtgtgctgtaagtttttagatcaattaggtgctaaattagttatttacttaccgtaaa 123
|||||
Db 67 ttgtgtgctgtaagtttttagatcaattaggtgctaaattagttatttacttaccgtaaa 126
|||||
QY 124 gaacgtagccgtaaagcgcttgaaataattattagaacaataataaccagagagcgac 183
|||||
Db 127 gaacgtagccgtaaagcgcttgaaataattattagaacaataataaccagagagcgac 186
|||||
QY 184 ttatatcaaatgtatttcaaacgagcgatgaagaggttatttaattggtttttgagcaaatggt 243
|||||

Db 187 ttatatcaaatgtatttcaaacgagcgatgaagaggttatttaattggttttgagcaaatggt 246
|||||
QY 244 aaagatgttgcaatattgattggtgtatatcatccaatcgcaatttgcataatgaagac 303
|||||
Db 247 aaagatgttgcaatattgattggtgtatatcatccaatcgcaatttgcataatgaagac 306
|||||
QY 304 ttacgagcgacttttctgaaacttcaacgtgaaggtctcttctgttagctcaagacattagt 363
|||||
Db 307 ttacgagcgacttttctgaaacttcaacgtgaaggtctcttctgttagctcaagacattagt 366
|||||
QY 364 tcttactcaatacaaatgtgtgctcaatgaagctaaaaaataataatccagaaggtggtgac 423
|||||
Db 367 tcttactcaatacaaatgtgtgctcaatgaagctaaaaaataataatccagaaggtggtgac 426
|||||
QY 424 attgttgcaacaacatatatttaggtggtgcaaatccagattcgaataataataatgtagtgg 483
|||||
Db 427 attgttgcaacaacatatatttaggtggtgcaaatccagattcgaataataataatgtagtgg 486
|||||
QY 484 gttgtaaacgagcgttagaagcaaatgttaaatatttagcattagcatttaggtctcgtat 543
|||||
Db 487 gttgtaaacgagcgttagaagcaaatgttaaatatttagcattagcatttaggtctcgtat 546
|||||
QY 544 aatattcgtgttaatgcgaatttcagctggttcccaatccgtacatttaagtcgaaggtgtg 603
|||||
Db 547 aatattcgtgttaatgcgaatttcagctggttcccaatccgtacatttaagtcgaaggtgtg 606
|||||
QY 604 gttggttcaatacaaatcttcaagaaatcgaagcgctgcaccttttaaacgtaacgtt 663
|||||
Db 607 gttggttcaatacaaatcttcaagaaatcgaagcgctgcaccttttaaacgtaacgtt 666
|||||
QY 664 gatcaagtagaagtaggttaaacacagcggtctacttrttaagtgaacttatcaagtgccgtt 723
|||||
Db 667 gatcaagtagaagtaggttaaacacagcggtctacttrttaagtgaacttatcaagtgccgtt 726
|||||
QY 724 acaggtgaaatatattcattgtagtagcggtattccacgcaataataaa 771
|||||
Db 727 acaggtgaaatatattcattgtagtagcggtattccacgcaataataaa 774
|||||

RESULT 8

PCT-US02-03987-8794
; Sequence 8794, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elittra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8794
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(771)
PCT-US02-03987-8794

Query Match 98.9%; Score 762.6; DB 1; Length 771;
Best Local Similarity 99.2%; Pred. No. 1.6e-175;
Matches 765; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 atgttaattcttgaaacaaacatatgtcatcgtgggaatcgctaatgaagcgtagtatt 60
|||||
Db 1 atgttaattcttgaaacaaacatatgtcatcgtgggaatcgctaatgaagcgtagtatt 60
|||||
QY 61 gctttgtgctgctaaagtttttagatcaaatgttgctaaattagttatttactaccgt 120
|||||

```
Db 61 gcttttggtgcgtctaaagtttagatcaattaggctcaaataggtagtattactaccgt 120
QY 121 aaagaacgtgacgtctaaagagcttgaaataattattagaacaattataaatacaacagaagcg 180
Db 121 aaagaacgtgacgtctaaagagcttgaaataattattagaacaattataaatacaacagaagcg 180
QY 181 cacttatatacaattgatgtctcaagcgatgaagaggttattaaatggttttgagcaaat 240
Db 181 cacttatatacaattgatgtctcaagcgatgaagaggttattaaatggttttgagcaaat 240
QY 241 gqtaagaatgttgcaataattgatgtgtatcatcattcaatccgactttgcttaataatgaa 300
Db 241 ggtcaagaagtgtgcaataattgatgtgtatcatcattcaatccgactttgcttaataatgaa 300
QY 301 gacttacgcggacgcttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 360
Db 301 gacttacgcggacgcttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 360
QY 361 agttcttactatcaacaatttgctcatgaagctaaataataatgacagaagtggt 420
Db 361 agttcttactatcaacaatttgctcatgaagctaaataataatgacagaagtggt 420
QY 421 acattgttgcaacaacattattagtggtgcgaattgcgaattgcgaattcaaaaattataatgtg 480
Db 421 agcattgttgcaacaacattattagtggtgcgaattgcgaattgcgaattcaaaaattataatgtg 480
QY 481 ggtgtgtctaaagcgagcttagaagcaaatgttaaatatttagcattagacttagtct 540
Db 481 ggtgtgtctaaagcgagcttagaagcaaatgttaaatatttagcattagacttagtcca 540
QY 541 gataatattcgcgttaagtgaatttcagctgtgtccaaatccgtacattaaagtcaaaagt 600
Db 541 gataatattcgcgttaagtgaatttcagctgtgtccaaatccgtacattaaagtcaaaagt 600
QY 601 gfggggtgttcaatacatttcaagaaatcgaagcggtgcacctttaaaacgtaac 660
Db 601 gfggggtgttcaatacatttcaagaaatcgaagcggtgcacctttaaaacgtaac 660
QY 661 gttgatcaagtagaagtagttaaagcagcggttacttrttaagtgaacttatcaagtggc 720
Db 661 gttgatcaagtagaagtagttaaagcagcggttacttrttaagtgaacttatcaagtggc 720
QY 721 gttacaggtgaaataattcatgtagatagcggattccacgcaattaaataa 771
Db 721 gttacaggtgaaataattcatgtagatagcggattccacgcaattaaataa 771
```

RESULT 9

```
US-09-815-242-8794
; Sequence 8794, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
```

```
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8794
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(771)
US-09-815-242-8794
```

```
Query Match 98.9%; Score 762.6; IB 31; Length 771;
Best Local Similarity 99.2%; Pred. No. 1.6e-175;
Matches 765; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 atgttaaatcttgaaacaaacacatattgcattcatcgtggaatcgctaaatgaagcgtatt 60
Db 1 atgttaaatcttgaaacaaacacatattgcattcatcgtggaatcgctaaatgaagcgtatt 60
QY 61 gcttttggtgcgtctaaagtttttagatcaatttagtgctaaatttagtatttactaccgt 120
Db 61 gcttttggtgcgtctaaagtttttagatcaatttagtgctaaatttagtatttactaccgt 120
QY 121 aaagaacgtgacgtctaaagagcttgaaataattattagaacaattataaatacaacagaagcg 180
Db 121 aaagaacgtgacgtctaaagagcttgaaataattattagaacaattataaatacaacagaagcg 180
QY 181 cacttatatacaattgatgtctcaagcgatgaagaggttattaaatggttttgagcaaat 240
Db 181 cacttatatacaattgatgtctcaagcgatgaagaggttattaaatggttttgagcaaat 240
QY 241 ggttaagatgttggaacattattgatggtgtatattcattcaatcgctattgctaataatgaa 300
Db 241 ggttaagatgttggaacattattgatggtgtatattcattcaatcgctattgctaataatgaa 300
QY 301 gacttacgcggacgcttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 360
Db 301 gacttacgcggacgcttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 360
QY 361 agttcttactatcaacaatttggtctcatgaagctcaaaaaataataatgacagaagtggt 420
Db 361 agttcttactatcaacaatttggtctcatgaagctcaaaaaataataatgacagaagtggt 420
QY 421 agcattgttgcaacaacatatttagtggtgcgaatttcgcaggttcacaaattataatgtgatg 480
Db 421 agcattgttgcaacaacatatttagtggtgcgaatttcgcaggttcacaaattataatgtgatg 480
QY 481 ggtgtgtctaaagcgagcttagaagcaaatgtttaaattatttagcattagacttagtct 540
Db 481 ggtgtgtctaaagcgagcttagaagcaaatgtttaaattatttagcattagacttagtcca 540
QY 541 gataatattcgcgttaagtgaatttcagctgtgtccaaatccgtacattaaagtcaaaagt 600
Db 541 gataatattcgcgttaagtgaatttcagctgtgtccaaatccgtacattaaagtcaaaagt 600
QY 601 gfggggtgttcaatacatttcaagaaatcgaagcggtgcacctttaaaacgtaac 660
Db 601 gfggggtgttcaatacatttcaagaaatcgaagcggtgcacctttaaaacgtaac 660
QY 661 gttgatcaagtagaagtagttaaagcagcggttacttrttaagtgaacttatcaagtggc 720
Db 661 gttgatcaagtagaagtagttaaagcagcggttacttrttaagtgaacttatcaagtggc 720
QY 721 gttacaggtgaaataattcatgtagatagcggattccacjcaattaaataa 771
Db 721 gttacaggtgaaataattcatgtagatagcggattccacjcaattaaataa 771
```

RESULT 10

US-10-072-851-8794
: Sequence 8794, Application US/10072851
: GENERAL INFORMATION:
: APPLICANT: Carr, Grant J.
: APPLICANT: Xu, H. Howard
: APPLICANT: Foulkes, J. Gordon
: APPLICANT: Zamudio, Carlos
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Kari L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Roemer, Terry
: APPLICANT: Jiang, Bo
: APPLICANT: Boone, Charles
: APPLICANT: Bussey, Howard
: TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
: TITLE OF INVENTION: Proliferation
: FILE REFERENCE: ELITRA.028A
: CURRENT APPLICATION NUMBER: US/10/072,851
: CURRENT FILING DATE: 2002-02-08
: PRIOR APPLICATION NUMBER: 60/267,636
: PRIOR FILING DATE: 2001-02-09
: NUMBER OF SEQ ID NOS: 15811
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8794
: LENGTH: 771
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(771)
US-10-072-851-8794

Query Match 98.9%; Score 762.6; DB 37; Length 771;
Best Local Similarity 99.2%; Pred. No. 1.6e-175;
Matches 765; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 atgttaaatcttgaaacaaacatatgtcatcgttggaatcgtaataagcgtagtatt 60
Db 1 atgttaaatcttgaaacaaacatatgtcatcgttggaatcgtaataagcgtagtatt 60
Qy 61 gcttttggtgcgctaagtttagatcaattaggtgtcctaattagttatttactaccgt 120
Db 61 gcttttggtgcgctaagtttagatcaattaggtgtcctaattagttatttactaccgt 120
Qy 121 aaagaacgtagccgtaaaagagcttgaaatatttagaacaattaaatcaaccagaagcg 180
Db 121 aaagaacgtagccgtaaaagagcttgaaatatttagaacaattaaatcaaccagaagcg 180
Qy 181 cacttatcaaatattgatgttcaaaagcgatgaagagttatttaattgagcaaat 240
Db 181 cacttatcaaatattgatgttcaaaagcgatgaagagttatttaattgagcaaat 240
Qy 241 ggtaaaagtgtggaataattgatgtgtatcatcattcgaatcgattgtcctaataatgaa 300
Db 241 ggtaaaagtgtggaataattgatgtgtatcatcattcgaatcgattgtcctaataatgaa 300
Qy 301 gacttacgcggaacgcttttctgaaacttcacgtgaaagccttctgttagctcgaagacatt 360
Db 301 gacttacgcggaacgcttttctgaaacttcacgtgaaagccttctgttagctcgaagacatt 360
Qy 361 agttcttactcaatacaaatgttggtcgtcatgaagctaaaaaatttaagccagaagtggt 420
Db 361 agttcttactcaatacaaatgttggtcgtcatgaagctaaaaaatttaagccagaagtggt 420
Qy 421 agcattgttgcacaaacatatattaggtggtggaattcgcagttcgaataatttaattgtagt 480
Db 421 agcattgttgcacaaacatatattaggtggtggaattcgcagttcgaataatttaattgtagt 480

Db 421 agcattgttgcacaaacatatattaggtggtggaattcgcagttcgaataatttaattgtagt 480
Qy 481 ggtgtgtctaaagcgagcttagaagcaaatgttaaatatttagcattagacttaggtcct 540
Db 481 ggtgtgtctaaagcgagcttagaagcaaatgttaaatatttagcattagacttaggtcct 540
Qy 541 gataatatctcgcttaattgcaatttcagctggtgccaatccgtacatttaagtgcaaaaggt 600
Db 541 gataatatctcgcttaattgcaatttcagctggtgccaatccgtacatttaagtgcaaaaggt 600
Qy 601 gtgggtgtgttcaatacaaatcttaaaagaaatcgaaagagcgtagcccttttaaacgtaac 660
Db 601 gtgggtgtgttcaatacaaatcttaaaagaaatcgaaagagcgtagcccttttaaacgtaac 660
Qy 661 gttgatacgaatagtaggtgaaacacagcggtcttacttrttaagtgaacttatcaagtgc 720
Db 661 gttgatacgaatagtaggtgaaacacagcggtcttacttrttaagtgaacttatcaagtgc 720
Qy 721 gttacaggtgaaatattcatgtatagatgcggtattccacgcgaataataa 771
Db 721 gttacaggtgaaatattcatgtatagatgcggtattccacgcgaataataa 771

RESULT 11

PCT-US99-19726-5
: Sequence 5, Application PC/TUS9919726
: GENERAL INFORMATION:
: APPLICANT: Human Genome Sciences, Inc. et al.
: TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
: FILE REFERENCE: PB484
: CURRENT APPLICATION NUMBER: PCT/US99/19726
: CURRENT FILING DATE: 1999-08-31
: EARLIER APPLICATION NUMBER: 60/098,964
: EARLIER FILING DATE: 1998-09-01
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 916
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
PCT-US99-19726-5

Query Match 98.7%; Score 761; DB 1; Length 916;
Best Local Similarity 99.1%; Pred. No. 4.1e-175;
Matches 764; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 atgttaaatcttgaaacaaacatatgtcatcgttggaatcgtaataagcgtagtatt 60
Db 96 atgttaaatcttgaaacaaacatatgtcatcgttggaatcgtaataagcgtagtatt 155
Qy 61 gcttttggtgcgctaagtttagatcaattaggtgtcctaattagttatttactaccgt 120
Db 156 gcttttggtgcgctaagtttagatcaattaggtgtcctaattagttatttactaccgt 215
Qy 121 aaagaacgtagccgtaaaagagcttgaaatatttagaacaattaaatcaaccagaagcg 180
Db 216 aaagaacgtagccgtaaaagagcttgaaatatttagaacaattaaatcaaccagaagcg 275
Qy 181 cacttatcaaatattgatgttcaaaagcgatgaagagttatttaattgagcaaat 240
Db 276 cacttatcaaatattgatgttcaaaagcgatgaagagttatttaattgagcaaat 335
Qy 241 ggtaaaagtgtggaataattgatgtgtatcatcattcgaatcgattgtcctaataatgaa 300
Db 336 ggtaaaagtgtggaataattgatgtgtatcatcattcgaatcgattgtcctaataatgaa 395
Qy 301 gacttacgcggaacgcttttctgaaacttcacgtgaaagccttctgttagctcgaagacatt 360
Db 396 gacttacgcggaacgcttttctgaaacttcacgtgaaagccttctgttagctcgaagacatt 455
Qy 361 agttcttactcaatacaaatgttggtcgtcatgaagctaaaaaatttaagccagaagtggt 420
Db 361 agttcttactcaatacaaatgttggtcgtcatgaagctaaaaaatttaagccagaagtggt 420

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Db 456 agttcttactcattacaatttggtgctcatgaagctaaataataatgcccagaagtggt 515
QY 421 agcattgttgcaacaacatatttagtggtgcgaattcgcagttcacaataataatgtgatg 480
Db 516 agcattgttgcaacaacatatttagtggtgcgaattcgcagttcacaataataatgtgatg 575
QY 481 ggtgttgctaaagcagcttagaagcaaatgttaataattattagcatttagcttagtct 540
Db 576 ggtgttgctaaagcagcttagaagcaaatgttaataattattagcatttagtcttagtcca 635
QY 541 gataatattcgcgttaataatcgaattcagctggtcccaatcgcgtacatttaagtgcgaaggt 600
Db 636 gataatattcgcgttaataatcgaattcagctggtcccaatcgcgtacatttaagtgcgaaggt 695
QY 601 gttggtgttgctaaacataatcttaagaataatcgaagagcgtgcacctttaaacgtaac 660
Db 696 gttggtgttgctaaacataatcttaagaataatcgaagagcgtgcacctttaaacgtaac 755
QY 661 gttgatacagtagaagtagttaaagcagcgttactttrtaagtgaacttacaagtggc 720
Db 756 gttgatacagtagaagtagttaaagcagcgttactttrtaagtgaacttacaagtggc 815
QY 721 gttacaggtgaaataattcatgtagatagcggattccacgcgaattaaataa 771
Db 816 gttacaggtgaaataattcatgtagatagcggattccacgcgaattaaataa 866

RESULT 12
US-09-512-255-5
; Sequence 5, Application US/09512255
; GENERAL INFORMATION:
; APPLICANT: Bailey et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PB484P1
; CURRENT APPLICATION NUMBER: US/09/512,255
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: PCT/US99/19726
; EARLIER FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: 60/098,964
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-512-255-5

Query Match 98.7%; Score 761; DB 19; Length 916;
Best Local Similarity 99.1%; Pred. No. 4.1e-175;
Matches 764; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 atgttaaatcttgaaacaaacatatgtcatcatggaatcgtaataagcgtagtatt 60
Db 96 atgttaaatcttgaaacaaacatatgtcatcatggaatcgtaataagcgtagtatt 155
QY 61 gcttttggtgcgtcaaaagtcttgatcaattagtgctgctaaatttagtatttaccgt 120
Db 156 gcttttggtgcgtcaaaagtcttgatcaattagtgctgctaaatttagtatttaccgt 215
QY 121 aagaacgtagcgtgaaagcgttgaaataattattagaacaaatttaataacacagaagc 180
Db 216 aagaacgtagcgtgaaagcgttgaaataattattagaacaaatttaataacacagaagc 275
QY 181 cacttatacaattatgttcaaacgtagaagaggttatttaattgtttgagcaaat 240
Db 276 cacttatacaattatgttcaaacgtagaagaggttatttaattgtttgagcaaat 335
QY 241 ggtaaagattgtggcaattatgtatcattcaatcgcatttgcataatggaa 300
Db 336 ggtaaagattgtggcaattatgtatcattcaatcgcatttgcataatggaa 395
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QY 301 gacttacgoggagcgtttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 360
Db 396 gacttacgoggagcgtttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 455
QY 361 agttcttactcattacaatttggtgctcatgaagctaaataataatgcagaagtggt 420
Db 456 agttcttactcattacaatttggtgctcatgaagctaaataataatgcagaagtggt 515
QY 421 agcattgttgcaacaacatatttagtggtgcgaattcgcagttcacaataataatgtgatg 480
Db 516 agcattgttgcaacaacatatttagtggtgcgaattcgcagttcacaataataatgtgatg 575
QY 481 ggtgttgctaaagcagcttagaagcaaatgttaataattattagcatttagcttagtct 540
Db 576 ggtgttgctaaagcagcttagaagcaaatgttaataattattagcatttagtcttagtcca 635
QY 541 gataatattcgcgttaataatcgaattcagctggtcccaatcgcgtacatttaagtgcgaaggt 600
Db 636 gataatattcgcgttaataatcgaattcagctggtcccaatcgcgtacatttaagtgcgaaggt 695
QY 601 gttggtgttgctaaacataatcttaagaataatcgaagagcgtgcacctttaaacgtaac 660
Db 696 gttggtgttgctaaacataatcttaagaataatcgaagagcgtgcacctttaaacgtaac 755
QY 661 gttgatacagtagaagtagttaaagcagcgttactttrtaagtgaacttacaagtggc 720
Db 756 gttgatacagtagaagtagttaaagcagcgttactttrtaagtgaacttacaagtggc 815
QY 721 gttacaggtgaaataattcatgtagatagcggattccacgcgaattaaataa 771
Db 816 gttacaggtgaaataattcatgtagatagcggattccacgcgaattaaataa 866

RESULT 13
US-09-512-255A-5
; Sequence 5, Application US/09512255A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PB484
; CURRENT APPLICATION NUMBER: US/09/512,255A
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/098,964
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/19726
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-512-255A-5

Query Match 98.7%; Score 761; DB 19; Length 916;
Best Local Similarity 99.1%; Pred. No. 4.1e-175;
Matches 764; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 atgttaaatcttgaaacaaacatatgtcatcatggaatcgtaataagcgtagtatt 60
Db 96 atgttaaatcttgaaacaaacatatgtcatcatggaatcgtaataagcgtagtatt 155
QY 61 gcttttggtgcgtcaaaagtcttgatcaattagtgctgctaaatttagtatttaccgt 120
Db 156 gcttttggtgcgtcaaaagtcttgatcaattagtgctgctaaatttagtatttaccgt 215
QY 121 aagaacgtagcgtgaaagcgttgaaataattattagaacaaatttaataacacagaagc 180
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Db 216 aaagaacgtagcgttaaagagcgttgaaataattattagaaacaattaaatcaaacagaaagcg 275
QY 181 cacttatatacaattgatgttcaagcgatgaagaggttatttaattggtttgagcaaat 240
Db 276 cacttatatacaattgatgttcaagcgatgaagaggttatttaattggtttgagcaaat 335
QY 241 ggttaagatgttggcaataattgataggtgtatatacatcaatcgaatttgcataatgaa 300
Db 336 ggttaagatgttggcaataattgataggtgtatatacatcaatcgaatttgcataatgaa 395
QY 301 gacttacgcggagcgttttctgaacttcacgtgaagccttcctgttagctcaagacatt 360
Db 396 gacttacgcggagcgttttctgaacttcacgtgaagccttcctgttagctcaagacatt 455
QY 361 agttcttactcaataatttggtcgtcatgaagcgttaaaaaattaatgcagaaagtggt 420
Db 456 agttcttactcaataatttggtcgtcatgaagcgttaaaaaattaatgcagaaagtggt 515
QY 421 agcattgttgcaacaacattattagttggcgaaattcgaggttcaaaaattataatgtatg 480
Db 516 agcattgttgcaacaacattattagttggcgaaattcgaggttcaaaaattataatgtatg 575
QY 481 ggtgtgtcaaaagcgagcttagaagcaaatgttaaatatttagcattagacttagtct 540
Db 576 ggtgtgtcaaaagcgagcttagaagcaaatgttaaatatttagcattagacttagtct 635
QY 541 gataatattcgcgttaattgcaatttcagctggttccaatccgtacatttaagtcaaaaggt 600
Db 636 gataatattcgcgttaattgcaatttcagctggttccaatccgtacatttaagtcaaaaggt 695
QY 601 gtgggtgttttcaatcacattcttaaaagaaatcgaaagcgtgcacctttaaaacgtaac 660
Db 696 gtgggtgttttcaatcacattcttaaaagaaatcgaaagcgtgcacctttaaaacgtaac 755
QY 661 gtgatcaagtagaagtaggttaaaacagcggcttacttirtaagtgcattatcaagtgac 720
Db 756 gtgatcaagtagaagtaggttaaaacagcggcttacttirtaagtgcattatcaagtgac 815
QY 721 gttacaggtgaaatattcatgtagatagcgggattccacgcaattataaa 771
Db 816 gttacaggtgaaatattcatgtagatagcgggattccacgcaattataaa 866

RESULT 14
PCT-US00-12104-1
; Sequence 1, Application PC/TUS0012104
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS
; FILE REFERENCE: GM50056
; CURRENT APPLICATION NUMBER: PCT/US00/12104
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 775
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
PCT-US00-12104-1

Query Match 98.1%; Score 756.6; DB 1; Length 775;
Best Local Similarity 99.5%; Pred. No. 4.6e-174;
Matches 771; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 atgttaaatcttgaaacaaacattatgtcatcatggtggaatcgcttaataagcgtagtatt 60
Db 1 atgttaaatcttgaaacaaacattatgtcatcatggtggaatcgcttaataagcgtagtatt 60
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QY 61 gcttttggtcgtctaaagtttttagatcatcaattaggctgctaaatttagtatttaccgt 120
Db 61 gcttttggtcgtctaaagtttttagatcaattaggctgctaaatttagtatttaccgt 120
QY 121 aaagaacgtagcgttaaagagcgttgaaaaattattagaacaattataatcaaacagaaagcg 180
Db 121 aaagaacgtagcgttaaagagcgttgaaaaattattagaacaattataatcaaacagaaagcg 180
QY 181 cacttatatacaattgatgttcaaaagcgtatgaagaggttattcaatggttttggagcaaat 240
Db 181 cacttatatacaattgatgttcaaaagcgtatgaagaggttattcaatggttttggagcaaat 240
QY 241 ggttaagatgttggcaataattgatgtgtatatacatcaatcgaatttgcataatgaa 300
Db 241 ggttaagatgttggcaataattgatgtgtatatacatcaatcgaatttgcataatgaa 300
QY 301 gacttacgcggagcgttttctgaacttcacgtgaagccttcctgttagctcaagacatt 360
Db 301 gacttacgcggagcgttttctgaacttcacgtgaagccttcctgttagctcaagacatt 360
QY 361 agttcttactcaataatttggtcgtcatgaagcgttaaaaaattaatgcagaaagtggt 420
Db 361 agttcttactcaataatttggtcgtcatgaagcgttaaaaaattaatgcagaaagtggt 420
QY 421 agcattgttgcaacaacattattagttggcgaaattcgaggttcaaaaattataatgtatg 480
Db 421 agcattgttgcaacaacattattagttggcgaaattcgaggttcaaaaattataatgtatg 480
QY 481 ggtgtgtcaaaagcgagcttagaagcaaatgttaaatatttagcattagacttagtct 540
Db 481 ggtgtgtcaaaagcgagcttagaagcaaatgttaaatatttagcattagacttagtct 540
QY 541 gataatattcgcgttcaattgcaatttcagctggttccaatccgtacatttaagtgcataaggt 600
Db 541 gataatattcgcgttcaattgcaatttcagctggttccaatccgtacatttaagtgcataaggt 600
QY 601 gtgggtgttttcaatcacattcttaaaagaaatcgaaagcgtgcacctttt----aaaacg 656
Db 601 gtgggtgttttcaatcacattcttaaaagaaatcgaaagcgtgcaccttttguraaaaacg 660
QY 657 taacgtgtatcaagtagaagtaggttaaaacagcggcttacttirtaagtgcattatcaag 716
Db 661 taacgtgtatcaagtagaagtaggttaaaacagcggcttacttirtaagtgcattatcaag 720
QY 717 tggcgttacaggtgaaatattcatgtagatagcgggattccacgcaattataaa 771
Db 721 tggcgttacaggtgaaatattcatgtagatagcgggattccacgcaattataaa 775

RESULT 15
US-10-009-219-1
; Sequence 1, Application US/10009219
; GENERAL INFORMATION:
; APPLICANT: DEWOLF, WALTER E.
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS
; FILE REFERENCE: GM50056
; CURRENT APPLICATION NUMBER: US/10/009,219
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PCT/US00/12104
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/134,362
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 775
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-009-219-1

Query Match 98.1%; Score 756.6; DB 37; Length 775;
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